

From: Hutzell, Paula
Sent: Wednesday, September 01, 2004 3:39 PM
To: Graser, Jennifer; STIC-Biotech/ChemLib
Subject: RE: rush search

approved

-----Original Message-----

From: Graser, Jennifer
Sent: Wednesday, September 01, 2004 3:13 PM
To: Hutzell, Paula
Subject: rush search
Importance: High

Hi Paula,
Could you please authorize this rush search for an Election?
Thanks, Jennifer

STIC:
Please search jnucleotides 918-1580 of SEQ ID NO: 12from 10/625,221 in
pending and commercial databases.

Thanks,
Jennifer Graser
REM 3B09 (mailbox 3C18)
Art Unit 1645
272-0858

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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1 (bases 1 to 821)
REFERENCE
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencing : BP 191 91.006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Marmoset in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
LOCATION http://bacpac.med.buffalo.edu/drosophila_bac.htm

source 1. 821 /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/mol

more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/clusterv.cgi?seq=CSGCAP008BD12NP1&cluster=534>. r. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genosope sequence ID : CSGCAP008BD12NP1.

FEATURES

Location/Qualifiers

source

1 /organism="Homo sapiens"

/mol_type="DNA"

/db_xref="taxon:9606"

/clone="CSGCAP008TG24"

/issue_type="THYMUS"

/clone.Lib="Homo sapiens THYMUS"

(note="vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo (GT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized." ORIGIN

Query Match 10.0%; Score 66; DB 13; Length 1200;

Best Local Similarity 43.8%; Pred. No. 0.0074; Matches 182; Conservative 31; Mismatches 206; Indels 2; Gaps 1;

QY 134 ATTATATAATATGTTCAGGCCAAATTATGATAAATAAACTGAACCTAAAGAACCC 193

Db 684 WTTTWWAAAYAATWTTATATAAAAMATAAAATTAAATAAWTTAWAAAMA 625

QY 194 AAGAGATGGCAACTTATTAAAGGATAAAACGTTGATATTATGGTAGAAATTATTAC 253

Db 624 AAAATAATAAAATAAAATAAAWAAAATAAAATAAAATAAAATAAAATAAAATA 565

QY 254 ATCTCTGTATTATGTAATGCAAGGATGCCATGTATCTAGCAGGGTAACCA 313

Db 564 TAAATAWAAAMAATTTNAAMATAATTAATAAAATAAAATAAAATAAAATA 505

QY 314 ATCATGAGGGAATCATTAGATAATCCTAAAGGATAGTCGTAAAGPATCAATCGATG 373

Db 504 ATAATCAA-T-AATWAAAATAWAAAATAATAATAATAATAATAATAATA 447

QY 374 GSTATCCAAAGCTCATTTGTATATTGAAACAATAAAATAATGGTAACCTGCTCAAGAAT 433

Db 446 TTAAAAATAATATNWAAAATAAAATAAAATAAAATAAAATAAAATAAAATA 387

QY 434 TAGACTTAAAGTTGAAATAATCTTACAGATAATAAGGAACTATATAATGGACCTT 493

Db 386 WTAAAATAATATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATA 327

QY 494 CTAAATATAAACTGGATATAAAAGTTTACACTGATAACGATAAAGGAAATGGTTGGTTG 553

Db 326 ANMMATAAAMMMTTTAATTACCATMATAAKTTICAACACTTACGCCAGATTGGGTITG 267

QY 554 A 554

Db 266 A 266

QY 264 AACCTTATTAAAGGATAAACGTTGATTTATGGTAGATAATTTACCATCTCTGTAA 263

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QY 265 TTTATGAAATTCCTAAAGGACTTAAAGGATTTTAAAGGAAATTTAAAGGAAATTT 662

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RESULT 15
CNS0039G CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
AL063921 of RPCI-88 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL063921 GI:4941778

KEYWORDS GSS.
Drosophila melanogaster (fruit fly)

ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriidae; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT - Web : www.genoscope.cns.fr).
The BDGP BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammober in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BAC4C Resource Center can be
found at http://bapac.med.buffalo.edu/drosophila_bac.htm.

FEATURES source
/organism="Drosophila melanogaster"
/mol type="Genomic DNA"
/db_xref="URAXON:7227"
/clon="BACR08K10"
/clone lib="RPCI-98"
/note="end : TET3"

ORIGIN

Query Match 9.9% Score 65.8 DB 29 Length 1101;
Best Local Similarity 21.9% Prd. No. 0.0083;
Matches 115; Conservative 198; Mismatches 211; Indels 1; Gaps 1;

QY 138 AATATATAATGTTCAGGGCCAAATTAGATAAATTAAACTGAACCTTAAGAACCGAGA 197
Db 395 MATATAAWWWWWTTTTTAWAAAATAATTWWAAWAAAATAATTWWAAWAA 454

QY 198 GATGCGCAACTTATTAGGATAAAAAGTTGATATTATGGGTGATAATAACCACCT 257
Db 455 AAATWWTTTAWWWTTAWAAAATAAAAATAATTWWTTTAWWWTTAWWWTTA 514

QY 258 CTGTGATTATGCAAAATGCGAAGGAGTGCGATGTATCTACGGAGGGTAAACATCA 317
Db 515 AAATAAAAAAAAWAAAATAATAATTWWTTTAWWWTTAWWWTTAWWWTTA 574

QY 318 TGAGGGAAATCATTTAGAAATTCTAAAGATAAGTGCCTTAAGTCAATCGATGGTAT 377
Db 575 YTTTYTYYTWTMWEHTNMYTHAYAHHTWWHHTWWHMTWWHMTWWHWT 633

QY 378 CCAAAGCTATCATTTGATATTGAAACAAATAAAAATGGTAACGTCTCAAGAATAGA 437

Db 634 TYTAAYYYYYTCMYYYHMMHHHAHAHAHAAWWTTWTHAYHWAHYYYYYMCAMCM 693
QY 438 CTATAAGTTAGAAAATCTACAGATAAATAGCAACTATACTATGACCTCTCAA 497
Db 694 CTHCHCCYYHHTTAHHTTHWTAHYWWYWWYCTACTYHYHHHYHWAY 753

QY 498 ATATGAAACTGGATATAAAGTCATACCTAAAGATAAAGTTGTTGTTGATT 557
Db 754 HTTWYAWAHAMMMWHBAHYAAAATAAWAATTHYHHTTHYHMMYCCYNCTY 813
QY 558 TTCCCTGAACTTACTCAATTAATCTATGATAAGATAAAGTTGTTGTTGTTGATT 617
Db 814 HCWHYHTAYTCWTWWHWWWWHWWHHTWWHHTWWHHTWWHHTWWHHTWWHHTWWA 873

QY 618 GCTGACTCAAACACAAGCCAAATTGAGACTCTAACACAAACCAA 662
Db 874 THWACMTMHWWHWWMEHHRNACHAHHHTMCCHHMHCTCHH 918

Search completed: September 3, 2004, 18:56:46
Job time : 2413 secs

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OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 17:19:26 ; Search time 77 Seconds
 (without alignments)
 4778.343 Million cell updates/sec

Title: US-10-625-221-12_COPY_918_1580

Perfect score: 663

Sequence: 1 caaacagaccggatccaaag.....aatgttacctaacaacaaag 663

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents NA.*
 1: /cgn2_6/prodata/2/ina/5A_COMB.seq:
 2: /cgn2_6/prodata/2/ina/5B_COMB.seq:
 3: /cgn2_6/prodata/2/ina/6A_COMB.seq:
 4: /cgn2_6/prodata/2/ina/6B_COMB.seq:
 5: /cgn2_6/prodata/2/ina/pcrtus_COMB.seq:
 6: /cgn2_6/prodata/2/ina/backfiles.seq:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	663	100.0	1851	4	US-08-973-391C-12	Sequence 12, Appl
2	661.4	99.8	1837	3	US-08-943-537B-33	Sequence 33, Appl
3	661.4	99.8	1837	3	US-08-926-840B-33	Sequence 33, Appl
4	658.2	99.3	1837	4	US-08-144-776B-15	Sequence 15, Appl
5	166.8	25.2	773	2	US-08-446-918A-1	Sequence 1, Appl
6	166.8	25.2	773	2	US-08-580-806-1	Sequence 1, Appl
7	166.8	25.2	1712	4	US-09-144-776B-5	Sequence 5, Appl
8	164.2	24.8	1095	4	US-09-144-776B-13	Sequence 13, Appl
9	158.8	24.0	723	4	US-09-350-755A-3	Sequence 3, Appl
10	158.8	24.0	801	4	US-09-350-755A-2	Sequence 1, Appl
11	158.8	24.0	1388	4	US-09-144-776B-9	Sequence 9, Appl
12	158.8	24.0	1712	4	US-09-144-776B-7	Sequence 7, Appl
13	112	16.9	815	4	US-09-414-276-7	Sequence 12, Appl
14	71	10.7	757	4	US-09-144-776B-3	Sequence 3, Appl
15	71	10.7	757	4	US-09-350-755A-1	Sequence 1, Appl
16	71	10.7	830	4	US-09-144-776B-1	Sequence 1, Appl
17	66.2	10.0	675	4	US-08-956-171E-887	Sequence 887, Appl
18	62.2	9.4	1789	4	US-08-936-165A-116	Sequence 116, Appl
19	59	8.9	751	1	US-08-446-918A-3	Sequence 3, Appl
20	59	8.9	640681	4	US-08-580-806-3	Sequence 3, Appl
21	52.4	7.9	640681	4	US-09-790-888-1	Sequence 1, Appl
22	50.8	7.7	19124	4	US-08-497-826B-13	Sequence 13, Appl
C 23	48.6	7.3	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 24	48.4	7.3	4185	4	US-09-417-485D-7	Sequence 7, Appl
C 25	48.4	7.3	10640	4	US-09-417-485D-5	Sequence 5, Appl
C 26	47.6	7.2	1887	4	US-09-601-198-39	Sequence 39, Appl
C 27	47.6	7.2	610681	4	US-09-790-988-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
 US-08-973-391C-12
 ; Sequence 12, Application US/08973391C
 ; Patent No. 652441
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlievert, Patrick M.
 ; APPLICANT: Roggiani, Manuela
 ; APPLICANT: Stoehr, Jennifer
 ; APPLICANT: Ohlendorf, Douglas
 ; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
 ; FILE REFERENCE: 600_311USWO
 ; CURRENT APPLICATION NUMBER: US/08/973,391C
 ; CURRENT FILING DATE: 1999-03-12
 ; PRIORITY APPLICATION NUMBER: PCT/US96/10252
 ; PRIORITY FILING DATE: 1996-06-07
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 1851
 ; TYPE: DNA
 ; ORGANISM: Streptococcus pyogenes
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (828)..(1583)
 ; OTHER INFORMATION:
 ; US-08-973-391C-12

Query Match Best Local Similarity 100.0% Score 663; DB 4; Length 1851;
 Matches 663; Conservative 0; Missmatches 0; Indels 0; Gaps 0;

QY 1 CAACAGACCCCCATGCCAGCAACTTCAGAGTCATTAGTTAGTAACACCTTAAAT 60
 Db 918 CAACAGACCCCCATGCCAGCAACTTCAGAGTCATTAGTTAGTAACACCTTAAAT 977
 QY 61 ATATATTTCTTTATGAGGGTGAACCTGTNTACTCCGAGAATGTTAAATCTGTGATCA 120
 Db 978 ATATATTTCTTTATGAGGGTGAACCTGTNTACTCCGAGAATGTTAAATCTGTGATCA 1037
 QY 121 CTTTATCTCACCATTAAATATAATGTTTCAGGGCCAATTATGATAAATTAAACT 180
 Db 1038 CTTTATCTCACCATTAAATATAATGTTTCAGGGCCAATTATGATAAATTAAACT 1097
 QY 181 GAACTTAACACCAAGAGATGGCAGCTTAACTTAAAGGTTAAACCTTATGTTATGTT 240
 Db 1098 GAACTTAACACCAAGAGATGGCAGCTTAACTTAAAGGTTAAACCTTATGTTATGTT 1157
 QY 241 GTAGATAATTACCATCTCGTTATTATGTGAAAATGCGAAAGAGTCATCTPAC 300

SEQUENCE CHARACTERISTICS:
 LENGTH: 1837 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Streptococcus pyogenes
 US-08-743-637B-33

	Query Match	Score	DB	Length
	Best Local Matches	99.8%	661.4;	1837;
	Conservative Matches	99.8%	Pred. No. 2e-143;	
	0; Mismatches 1;	Indels 0;	Gaps 0;	
QY	1 CAAAGAACCCGATCCAGGCAACTTCACAGATCTACTTAAACCTCAAAAT	60		
Db	904 CAACAGACCCCGATCCAGGCAACTTCACAGATCTACTTAAACCTCAAAAT	963		
QY	61 ATATATTTCTTTATGAGGTGACCCGTTACTCAGGAAATCTGAAATCTGTGATAA	120		
Db	964 ATATATTTCTTTATGAGGTGACCCGTTACTCAGGAAATCTGAAATCTGTGATAA	1023		
QY	121 CTTTTATCTCACCATTAAATAATATGAACTGGCAAATTATGATAAATTAAACT	180		
Db	1024 CTTTATCTCACCATTAAATAATATGAACTGGCAAATTATGATAAATTAAACT	1083		
QY	181 GAACTTAAGAACCAAGAGATGGCACTTTAAAGGATAAAAGCTGTGATTTATGT	240		
Db	1084 GAACTTAAGAACCAAGAGATGGCACTTTAAAGGATAAAAGCTGTGATTTATGT	1143		
QY	241 GTGACATATTACCATCTCTGTTATTATGAAATGGAGTGATCTATCTPAC	300		
Db	1144 GTGACATATTACCATCTCTGTTATTATGAAATGGAGTGATCTATCTPAC	1203		
QY	301 GGAGGGTACAAATCATGAGGAACTTAAAGTAGCTTAA	360		
Db	1204 GGAGGGTACAAATCATGAGGAACTTAAAGTAGCTTAA	1263		
QY	361 GTATCAATCGATGGTATCCAAAGCTATGATTCGAAATAAAAGTGTAA	420		
Db	1264 GTATCAATCGATGGTATCCAAAGCTATGATTCGAAATAAAAGTGTAA	1323		
QY	421 ACTGCTCAGAAATTGACTTAAAGTTGAACTATGAACTATGAACTATAT	480		
Db	1324 ACTGCTCAGAAATTGACTTAAAGCTATGATTCGAAATAAAAGTGTAA	1382		
QY	481 ACTATGGACCTTCTAAATGAACTTAAAGTTCATCTTAAAGAA	540		
Db	1384 ACTATGGACCTTCTAAATGAACTTAAAGTTCATCTTAAAGAA	1441		
QY	541 AGTTTTGGTTGATTTTCCCTGAAACCAAAATTACTCAATCTAAATCTGTATA	600		
Db	1504 TATAAGATAATGAAACCTAACACACGCTTGACCTAACACC	1562		
QY	661 AAG 663			
Db	1564 AAG 1566			

RESULT 3
 US-08-526-840B-33
 Sequence 33, Application US/08526840B3
 GENERAL INFORMATION:
 Patent No. 5994066
 APPLICANT: BERGERON, Michel G.
 APPLICANT: PICARD, Francois J.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED TITLES OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED TITLES OF INVENTION: ANTI-BIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:
 ADDRESS: QUARLES & BRADY
 STREET: 411 EAST WISCONSIN AVENUE
 CITY: MILWAUKEE
 STATE: WISCONSIN
 COUNTRY: USA
 ZIP: 53202-4497
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/743,637B
 FILING DATE: 04-NOV-1996
 PRIORITY APPLICATION NUMBER: US 08/526,840
 CLASSIFICATION: -435
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 TELECOMMUNICATION INFORMATION:
 REGISTRATION NUMBER: 35-133
 NAME: BAKER, Jean C.
 FILING DATE: 11-SEP-1995
 TELEPHONE: (414) 277-5591
 INFORMATION FOR SEQ ID NO: 33:

RESULTS
 Sequence 33, Application US/08526840B3
 Patent No. 6001564
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED TITLES OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED TITLES OF INVENTION: ANTI-BIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:
 ADDRESS: QUARLES & BRADY
 STREET: 411 EAST WISCONSIN AVENUE
 CITY: MILWAUKEE
 STATE: WISCONSIN
 COUNTRY: USA
 ZIP: 53202-4497
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/743,637B
 FILING DATE: 04-NOV-1996
 PRIORITY APPLICATION NUMBER: US 08/526,840
 CLASSIFICATION: -435
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 TELECOMMUNICATION INFORMATION:
 REGISTRATION NUMBER: 35-133
 NAME: BAKER, Jean C.
 FILING DATE: 11-SEP-1995
 TELEPHONE: (414) 277-5591
 INFORMATION FOR SEQ ID NO: 33:

TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
 NUMBER OF SEQUENCES: 157
 CORRESPONDENCE ADDRESS:
 QUARLES & BRADY
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/526, 840B
 FILING DATE: 11-SEP-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/304, 732
 FILING DATE: 12-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586-90012
 TELEPHONE: (414) 277-5000
 TELEFAX: (414) 277-5591
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1837 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: Linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: streptococcus pyogenes
 US-08-526-840B-33

Query Match 99.8%; Score 661.4; DB 3; Length 1837;
 Best Local Similarity 99.8%; Pred. No. 2e-143;
 Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAACAGAACCGATCAAGCCAACCTCACAGATCTACTTTAGTTAAACCTTCAAAAT 60
 Db 904 CAACAGAACCCGATCAAGCCAACCTCACAGATCTACTTTAGTTAAACCTTCAAAAT 963

QY 61 ATATATTCTTATAGGGTGACCCGTACTCAGGAATGTCAAATCTGTGATCAA 120
 Db 964 ATATATTCTTATAGGGTGACCCGTACTCAGGAATGTCAAATCTGTGATCAA 1023

QY 121 CTTTATCACCATTAAATATATGTTAGGCCAATTATGATAATTAAACT 180
 Db 1024 CTTTATCACCATTAAATATATGTTAGGCCAATTATGATAATTAAACT 1083

QY 181 GAACTTAAGAACCAAGAGATGGCAACTTAAAGGATAAAAGTAGTCGTTAACTGGT 240
 Db 1084 GAACCTAACGAAATGAGGAAATTAAAGGATAAAAAGTAGTCGTTAACTGGT 1143

QY 241 GTAGAATATTACCATCTCGTTATTATGCAAAGGAGTGTGATGATCTAC 300
 Db 1144 GTAGAATATTACCATCTCGTTATTATGCAAAGGAGTGTGATGATCTAC 1203

QY 301 GGAGGGTAAACATGAGGGAACTTAAAGGAAATTCCTAAAGGATGTTAA 360
 Db 1204 GGAGGGTAAACATGAGGGAACTTAAAGGATGTTAAAGGATGTTAA 1263

QY 361 GTATCAATGATGGTATCAAGGCCATATTGATAATGAAACAAATAAAAATGGTA 420
 Db 1264 GTATCAATGATGGTATCAAGGCCATATTGATAATGAAACAAATAAAAATGGTA 1323

QY 421 ACTGCTCAAGAATTAGACTATAAAGTTAGAAATATCTACAGATAATAGCAACTATAT 480

Db 1324 ACTGCTCAAGAATTAGACTATAAAGTTAGAAATATCTACAGATAATAGCAACTATAT 1383
 QY 481 ACTATGGACCTCTAAATGAAACTGATGATAATGAACTTAAGATAAGAA 540
 Db 1384 ACTATGGACCTCTAAATGAACTTAAGTCAACTTAAGATAAGAA 1443
 QY 541 AGTTTGGTTGATTTTCCCGAACCGAAATTACCAATCTAAATCTGTGATA 600
 Db 1444 AGTTTGGTTGATTTTCCCGAACCGAAATTACCAATCTAAATCTGTGATA 1503
 QY 601 TATAGATAATGAACTGCTGACTCAAACAGCCAAATTGAGTCTACCAACC 660
 Db 1504 TATAGATAATGAAACGCTGTGACTCAAACAGCCAAATTGAGTCTACCAACC 1563
 QY 661 AAG 663
 Db 1564 AAG 1566

RESULT 4
 US-09-144-776B-15
 Sequence 15, Application US/09144776B
 Patent No. 639932
 GENERAL INFORMATION:
 APPLICANT: Robert G. Ulrich,
 Mark A. Olson
 Sina Bavari
 TITLE OF INVENTION: Bacterial Superantigen
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Charles H. Harris
 STREET: US Army MRCM -504 Scott Street
 MCGR-JA (Charles H. Harris Patent
 Atty)
 CITY: FORT DETRICK
 STATE: MARYLAND
 COUNTRY: USA
 ZIP: 21702-5012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.5
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 NUMBER: US/09/144-776B
 FILING DATE: 01-Sep-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 NUMBER: 08/882,431
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Charles H. Harris
 REGISTRATION NUMBER: 34,616
 REFERENCE/DOCKET NUMBER: <Unknown>
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1837
 TYPE: Nucleic Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 US-09-144-776B-15

Query Match 99.3%; Score 658.2; DB 4;
 Best Local Similarity 99.5%; Pred. No. 1.e-142;
 Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CAAACAGACCCCCGATCCAGCCAACTCAGAGTCAGTTAGTTAAACCTTCAAAAT 60
 2 904 CAAACAGACCCCCGATCCAGCCAACTCAGAGTCAGTTAGTTAAACCTTCAAAAT 963
 3
 QY 61 ATATATTTCTTTATGGGGTGAACCGCTGTACTCAGGAAATCTGTGATCAA 120
 4 Db 964 ATATATTTCTTTATGGGGTGAACCGCTGTACTCAGGAAATCTGTGATCAA 1023
 5
 QY 121 CTTTATTCACATTATAATATAGTTAGGGCAAAATTGATAAATTAANAACT 180
 6 Db 1024 CTTAGATCTCAGGTTATATAATAGTTAGGGCAAAATTGATAAATTAANAACT 1083
 7
 QY 181 GAACTTAAAGAACAGAGATGGCAACTTTAAAGGATAAAAACCGTGATTTATGGT 240
 8 Db 1084 GAACTTAAAGAACAGAGATGGCAACTTTAAAGGATAAAAACCGTGATTTATGGT 1143
 9
 QY 241 GTAGAAATTACCATCTCTGTATTATGTGAAAAATSCGAAAGGACTGCATGTAC 300
 10 Db 1144 GTAGAAATTACCATCTCTGTATTATGTGAAAAATSCGAAAGGACTGCATGTAC 1203
 11
 QY 301 GGAGGGGTAAACAAATCATGAAAGCATTAGAACTTAAAGACATTCGTAA 360
 12 Db 1204 GGAGGGGTAAACAAATCATGAAAGCATTAGAAATTCCCTAAAGATCTCGTAA 1263
 13
 QY 361 GATCAATCGATGGTATCCAAGCCTATCATTTGATATTGAAACAAATAAAAATGTA 420
 14 Db 1264 GATCAATCGATGGTATCCAAGCCTATCATTTGATATTGAAACAAATAAAAATGTA 1323
 15
 QY 421 ACTGCTCAGAAATTAGACTATAAGTAGAAATTATCTTACAGATAAATAGGACTATAT 480
 16 Db 1324 ACTGCTCAGAAATTAGACTATAAGTAGAAATTATCTTACAGATAAATAGGACTATAT 1383
 17
 QY 481 ACTATGGACCTCTAAATATGAAACCGATATAAAGTCATACCTAAGGATAAAGAA 540
 18 Db 1384 ACTAATGGACCTCTAAATATGAAACCGATATAAAGTCATACCTAAGGATAAAGAA 1443
 19
 QY 541 AGTTTTGGTTGATTTCCCTGAAACCGGATTACTCAATCTTATCTTATATA 600
 20 Db 1444 AGTTTTGGTTGATTTCCCTGAAACCGGATTACTCAATCTTATCTTATATA 1503
 21
 QY 601 TATAAGATAATGAAACCGCTGACTCAAAACACAGCCAAATTGAAAGTGTACCTAACACC 660
 22 Db 1504 TATAAGATAATGAAACCGCTGACTCAAAACACAGCCAAATTGAAAGTGTACCTAACACC 1563
 23
 QY 661 AAG 663
 24 Db 1564 AAG 1566

RESULT 5
 US-08-446-918A-1
 Sequence 1, Application US/08446918A
 ; GENERAL INFORMATION:
 ; APPLICANT: Dow, Steve W.
 ; ADDRESS: Sheridan Ross & McIntosh
 ; STREET: 1700 Lincoln Street, Suite 3500
 ; CITY: Denver
 ; STATE: Colorado
 ; COUNTRY: U.S.A.
 ; ZIP: 80203
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patient Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,918A
 ; FILING DATE: 18-MAY-1995

CLASSIFICATION: 552
 ATTORNEY/AGENT INFORMATION:
 NAME: Kovarik, Joseph B.
 REGISTRATION NUMBER: 33,005
 REFERENCE/DOCKET NUMBER: 2879-29
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 773 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..778
 US-08-446-918A-1

Query Match 25.2%; Score 166.8; DB 1; Length 773;
 Best Local Similarity 59.1%; Pred. No. 9.4e-31;
 Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;

Qy 56 AAATATATATTTCTTTATGAGGGTACCCGTTACTCACAGAAATCTGAAATCTGTT 115
 Db 113 AAATATGAAACCTTGTGATATCATGATATAAGTTAAAGTTAATCATAG 172
 Qy 116 ATCAACTTTATCTCACCATTATAATATGTTAGGGCA-----AATTATG 166
 Db 173 ATCAATTCTCATACTTGACTATAATCTTATTANGACACTAATTAGGGATATTG 232
 Qy 167 ATTAATTTPAATGAACTTAAAGAACCAAGGATGGCAACTTTAAGGATAAACG 226
 Db 233 ATATATGTTGAGNCGAATTAAACAAAGATTAGTGTAAATAAAAGATAATTCAGTCG 292
 Qy 227 TGTATTTATTGTTGAAATATACCTCCTGTTATTGTTGAA-----275
 Db 293 TAGATGTTGTTGGATGTTAATTATTTATCATGTTATTGTTCTAAAAAAGGAATGATA 352
 Qy 276 -----TCGAAAGGAGTGCATGATCTACGGAGGGSTAACAAATGATG 319
 Db 353 TAATTGGCATGAACTGACAAACGAAAAACTGTGTATGGTTAATCTGAGATA 412
 Qy 320 AAGGAATCATTAGAAATTCCAAAAGATACTCGTAAAGTATCATGATGGTATCC 379
 Db 413 ATGAAACCAATTAGATAAATAGAATGTTACTGTGCGTATTGAGGGTAA 472
 Qy 380 AAGGCCDTATCATTTGATTTGAAACAAATAAALAAAATGTAACCTGTCAGAAATTGACT 439
 Db 473 ATTATATCCTTGTACCTAACTTAAAGTTGGTTGACTGTCAGAAATTGATTGATT 532
 Qy 440 ATAAGTTGAAATTCTTAAAGATAATAACCACTATACATAATGACCTCTAAAT 499
 Db 533 ACCTTAATCTGTCATCTATTGGGAAARATAAAACCTATGAAATTGACACTCGCCTT 592
 Qy 500 ATGAAACTGGATATAAAGTCATACCTAAGATAAAGAAAGTTGGTTGATTTT 559
 Db 593 ATGAAACGGATATAAATTTA-----GAAATGAAATGATATAAGATAATGATG 649
 Qy 560 TCCTGAAACGAG----AATTACTGAACTTAACTTATGATATAAAAGATAATG 613
 Db 650 TGCTGCAACGGAGATAAATTTGACCTATGAAATGATGACATAACGACATA 709
 Qy 614 AACGGTTGACTCAAACAGCCAAATTGAGGCTACCTAACACAAAG 663
 Db 710 ATGGTTGATCTAAAGATGCAAGATTGAGCTTCTTACGAAAG 759

RESULT 6
 US-08-380-806-1
 Sequence 1, Application US/08580806
 ; Patent No. 5935568

GENERAL INFORMATION:
 APPLICANT: Dow, Steve W.
 APPLICANT: Elmslie, Robyn E.
 APPLICANT: Potter, Terence A.
 TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESS: Sherman Ross & McIntosh
 STREET: 1700 Lincoln Street, Suite 3500
 CITY: Denver
 STATE: Colorado
 COUNTRY: U.S.A.
 ZIP: 80203
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/580,806
 FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2879-29-C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0230
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 773 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..768
 US-08-580-806-1

Query Match Score 166.8; DB 2; Length 773;
 Best Local Similarity 59.1%; Pred. No. 9.4e-30;
 Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;

Qy 56 AAAATAATAATTCTTATGAGGTGACCTGTACTACGAGAATCTGTG 115
 Db 113 AAAATAAAAGTTGTATGATAATCATGCAATAAACGTAACTATAG 172
 Qy 116 ATCAACTTATCTCACCATTAAATATAATGTTCAGGCCA-----AATATG 166
 Db 173 ATCAATTCTATACTTGTACTTAATATTCCTATAAGGACATACTGGATTAG 232
 Qy 167 ATAATTAATAACTGAACCTAAGACCAAGATGGCACTTTATTAGGATAAAACG 226
 Db 233 ATAATGTTGAGTCATTAAACAAAGATTAGCTATAAACAGATAATAG 292
 Qy 227 TTGATATTATGTTGAGTATAACCATTCTGTTATATGAA----- 275
 Db 293 TAGATGTTGGCTAAATTCTAAATGTTCTAAAACGGATGATA 352
 Qy 276 -----TGAGAAGGGAGTCATTACGGAGGGTACAAATCATG 319
 Db 353 TTAATTGGCATCAAATGCAAAACTGAAACTGTTAAAGTCAATGAGGATA 412
 Qy 320 AGGGAAATATTTAGAAATCCCTAAAAAGATAGTGTAAAGTCAATGATG 379
 Db 413 ATGGAAACCAATTGATAAAATAGAATTAGCTTGTGGTATGAGTAA 472
 Qy 380 AAAGCCTATATTGATGATGAAACAAATCCCTAAAGATAGTGTAAAGTCAATG 439
 Db 473 ATTATATCTTGTGAGTCACAACTAAATAGAATTAGCTGCTCAAGAATTAGT 532

Qy 440 ATTAAGTTAGAAATATCCTACAGATAATAAGCACTATACTAATGGACCTTCTAAAT 499
 Db 533 ACCTAATCGTCATATTGGAAATAAAACTCTGAACT 592
 Qy 500 ATGAAACTGGATATAAAGTCTACCTAAGATAAAGTTTGGTTGTTTT 559
 Db 593 ATGAAACGGGATATAAATTATA--GAAATGAGATACTGTTGGTATGACATGA 649
 Qy 560 TCCCGAACAG---ANTTATCAATCTAATCTATGATAATAAGTTAATG 613
 Db 650 TGCCGACCAAGGATAAAATTGACCAATCTAAATTATAATGTCATAATGCAATA 709
 Qy 614 AAACGTTGACTAAACAGCCAAATGAAAGTCACTPARAACCAAG 663
 Db 710 AAATGTTGATCTAAAGATGTGAGATGAAFTATCTAACGAAAG 759
 RESULT 7
 US-09-144-776B-5
 Sequence 5, Application US/09144776B
 Patent No. 639932
 GENERAL INFORMATION:
 APPLICANT: Robert G. Ulrich,
 Mark A. Olson
 Sina Bavari
 TITLE OF INVENTION: Superantigen
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Charles H. Harris
 STREET: US Army MRMC -504 Scott Street
 MCMR-JA (Charles H. Harris-Patent
 Atty)
 CITY: FORT DETRICK
 STATE: MARYLAND
 COUNTRY: USA
 ZIP: 21702-5012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.5
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/144,776B
 FILING DATE: 01-Sep-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/882,431
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Charles H. Harris
 REGISTRATION NUMBER: 34,616
 REFERENCE/DOCKET NUMBER: <Unknown>
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1712
 TYPE: Nucleic Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-144-776B-5
 Query Match Score 166.8; DB 4;
 Best Local Similarity 59.1%; Pred. No. 1.1e-29;
 Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;
 Qy 56 AAATATATATTCTTATGAGGTGACCTGTAACTGCTGAAATCTGTG 115
 Db 389 AACATGAAAGTTGATGATAATGAACTTGTGATGATAATGATAAACTGATA 448

RESULT 8
US-09-144-776B-13
; Sequence 13, Application US/09144-776B
; Patent No. 6393332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WMRNC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095
TYPE: Nucleic Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-144-776B-13

```

116 ATCAACTTTTCTCACCATTAATAATGTTAGGGCAA-----ATTATG 166
449 ATCAATTCTACTTGACTTAATTCTATTAGGAACATGTTAGGGATAATG 508
167 ATAATTAACCTGAACTTAAGAACAGATGGAACTTTTAAGGATAAAAACG 226
509 ATAATGTTGAGTCGAAATTAAAACAAAGATTAGGTAAATACAAAGATAATACG 568
QY 227 TGTATTTATGGTGTGAAATTACCATCTGTATTATGTGAAAA----- 275
Db 569 TAGATGTTGGCTAAATTATATCAATGTGTATTTCTAAACAAAGATA 628
QY 276 -----TCCAGAAAAGGGAGTCGATGTCTACCGAGGGTAACAATCTG 319
Db 629 TTAATTGCGATCAAACGAAACGAAACTGATGTTAGTGTGAAATGAGATA 688
QY 320 AAGGGAAATCATTAGAATTCTTAAAGAGATAGTCGTTAAAGTCAATCGATGGTATCC 379
Db 689 ATGGAACCAATTAGATAATTAGAATGATTACTGTGGGTATTGTGAAATGTTAAA 748
QY 380 AAAGCTPATCATTTGAAACATAAAAATGTAACTGCTCAAGAACTTACACT 439
Db 749 ATTATATCATTTGAACTTAACTTAAGAAAGGTGACTGCTCAAGAAATTGATT 808
QY 440 ATAAAGTTGAAATAATCCTTACAGATAAACGAACTTATACATAATGGACCTTCTAAAT 499
Db 809 ACCTAACCTGCACTATTGGTGAATAAAACTCTAACTTAACACTGCCT 868
QY 500 ATGAAACTGGATAATAAAGGTCATACCTAAAGATAAAAGAAAGTTTGTTGATTTT 559
Db 869 ATGAAACGGATAATAATTATA---GAATAAGGAAATGCTTGGTAGATGTA 925
QY 560 TCCCTGACCG----AATTTACTCATCTAAATCTTATGATATAAGATATG 613
Db 926 TGCTGTGACCGGGATAAATTGGCCAACTPAAATTAAATGATGACATA 985
QY 614 AACAGCTGACTCAAAGCAAGGCCAAATGAACTCTAACTAAACCGTAG 663
Db 986 AATGGTGTGATCTAAAGATGCGAAGTTGAAATTCTTACGACAAAG 1035

```

Query Match 24.8%; Score 164.2; DB 4; Length 1095;
Best Local Similarity 58.7%; Pred. No. 4e-29;
Matches 380; Conservative 0; Mismatches 228; Indels 39; Gaps 4;

Qy 56 AAAATAATATTCTCACCATTATAATAATGTTTCAGG-----GCAATTTGTTG 115
Db 263 AAAATAATGAAAGTTTATATGATGATCATTTATGCAACTAAAGTTAGCTGTAG 322
Qy 116 ATCAACTTTTCTCACCATTATAATAATGTTTCAGG-----GCAATTTGTTG 166
Db 323 ATAAATTAGGCGACATGATTATAACATTAGTGTATAAAACTGAAATAATTG 382
Qy 167 ATAATAAATAAAACCTGAACTTAAAGAACCTAGAGATGGAAACTTTAAGGATAAAACG 226
Db 383 ACAAGTCAAACAGAGTTAAATAACAGTTAGAAAGGAGTCAAAGGAACTAGTAG 442
Qy 227 TGTATTTATGGTGTGAAATTACCATCTCTGTTATT----- 268
Db 443 TGTATGTTGATGATGTTCAATTACTATGTAATACTGCAATTCTGTTATGTT 502
Qy 269 GTGAAAATGCAAGAAGGTGCTATGATCTAAGGGGTAAACAAATCATGAGGGATC 328
Db 503 GTAAAGTGTACGGTGGAAATAATTGTGTGTTGAGGAAATAACATGAGGAAACC 562
Qy 329 ATTAGAAAATTCTA-----AAAAGATAATGCTGTTAAAGTCAATCGATGGTATCCAA 382
Db 563 ACTTTGATAATGGGAACTTACAAATGTAACGTTAAAGTTGAAATAAMAGAAACA 622
Qy 383 GCCTATCATTTGATATGAAACAAATAAAAATGGTAACTGCTCAAGAAATTGAGCTAA 442
Db 623 CAATTTCCTTGAGTGCACGTTGAACTGATAAGGTAACGGTCAAGAACTGACATAA 682
Qy 443 AAGTTGAGAAAATTCTACAGATAATAGCAACATAATCTACTATGGACCTCTAAATG 502
Db 683 AAGCTTAGGAAATTCTTAAATTAAATAAAATTGTATGAGTTAACAGTTGACCATATG 742
Qy 503 AACTGGATATAAAATGAACTTCATCCATCTAAAGGTTTGGTTGATTTTC 562
Db 743 AACAGGATATAAAATTGAAATAACCTAAACGCAAATTCTGTTGATGATGTC 802
Qy 563 CTGAAACCG----AATTTACTCATCTAAATCTTATGATATAAGATATGAAA 616
Db 803 CTGACCAAGGGGATAAGTTGACCAATCTAAATTGTTGAGGTTGACAGCAATAAA 862
Qy 617 CGCTTGACTCAACACACAGGCCAAATTGAGCTACCTAACAAACCAAG 663
Db 863 CGGTGATCTAAAGTGTGAAAGATAAGTCCACCTAACAAAC 909

RESULT 9
US-09-144-776B-13
; Sequence 3, Application US/09144-776B
; Patent No. 663640
; GENERAL INFORMATION:
; APPLICANT: United States Army Medical Research Institute of Infectious Diseases

APPLICANT: Lee, John Scott
APPLICANT: Pushko, Peter
APPLICANT: Smith, Jonathan F.
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Vaccine Against Staphylococcus
FILE REFERENCE: Army-136
CURRENT APPLICATION NUMBER: US 09/350,755A
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/092,416
PRIOR FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Microsoft Word 97 (IBM compatible)
SEQ ID NO: 3
LENGTH: 723
TYPE: DNA
ORGANISM: *Staphylococcus aureus*
JS-09-350-755A-3

Query	Match	Score	DB	Length
Query	Match	24.0%	8	723;
Best Local Similarity	Pred. No.	58.3%	4;	
Matches 379	Mismatches	0;	6.4e-28;	
Conservative	Indels	226;	45;	Caps 4;
Y	56	AAATATAATTTCTTTATGAGGGTGAACCTGTACTCACGAGAATGTGAATCTGTG	115	
b	68	AAATATGAAAGTTGTATGATGATAATATGTATCAGCAATAAACGTTAAATCGTATAG	127	
Y	116	ATCAACTTTATCTACCATTAAATAATAATGTTTCAGGGCCA-----AATTATG	166	
b	128	ATCAATTTCGATACTTGACTTTGACTTAATACTCTATAAGGACACTAGTTAGGGRATTATG	187	
Y	167	ATAAATTAAAAGCTGAACTTAAGACAAGAGATGCCAACTTTATAAGGATAAAACG	226	
b	188	ATAATGTTGAGTCGATTTAAACAAAGATTAGCTGATAAAACCAAGATAATACG	247	
Y	227	TGATATTTATGGTGTAGATAATTACACATCTGTATTATGTGAAAA-----	275	
b	248	TAGATGTTGGAGCTATGCTTATATACTGTGCTTTCTAAAAAACGAAATGATA	307	
Y	276	-----TGCGAGRAAGGAGTCATGTATCTACGGAGGGTACAAATCATG	319	
b	308	TAATTCSCATAAACTGACAAACGAAAACCTGTATGTATGTTGTAATCTGCACATA	367	
Y	320	AGGGAAACATTAGAAATTCTAAAAGATACTAGTGGTTAAAGTATCAATCGATGGPATCC	379	
b	368	ATCGAAACCAATTAGATAATATAGAAAGTATTACTGTTCGGTATTGTGAGATGGAAAA	427	
Y	380	AAAGCCTATCATTGATATTGAAACAAATAAAAATGGTAACTCTGTCAGAATTAGACT	439	
b	428	ATTATTAATCTTGTACGGTACAACTATAAGAAAAGGTGACTCTCAGAAATTGATT	487	
Y	440	ATAAAAGTTGAAATAATCTTACAGATAATAAGCAACTATACTACTATGGACCTTCTAAAT	499	
b	488	ACCTAACCTGTCRCTATTGGTGAAAAATTAACCTPATGAATTAAACACTGCCCT	547	
Y	500	ATGAAACCTGGTATATAAGTTCATACCTTAAGAAATAAGAAAGTTGTGTTGATTTT	559	
b	548	ATGAAACGGGATATATAATTATA--GAAAATGAGAATAGCTTGTGTTGATGATGA	604	
Y	560	TCCCTGAACCG-----AATTTACTCACTTAATACTCTTATGATAATAAGATAATG	613	
b	605	TCCCTGGACCGAGATAATTGACCACTCTAAATTTAATGTTGATGCAATGCAATA	664	
Y	614	AAACGCTTGACTAAACAACTAAAGCCAATTGAAATCTACCTAACACCAAG	663	
b	665	AAATGGCTGATTGTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	711	

1 APPLICANT: Lee, John Scott
1 APPLICANT: Pushko, Peter
1 APPLICANT: Smith, Jonathan F.
1 APPLICANT: Ulrich, Robert G.
1 TITLE OF INVENTION: Vaccine Against Staphylococcus Intoxication
1 FILE REFERENCE: Army-L3
1 CURRENT APPLICATION NUMBER: US/09/350,755A
1 CURRENT FILING DATE: 1998-07-09
1 PRIOR APPLICATION NUMBER: US 60/092,416
1 PRIOR FILING DATE: 1998-07-10
1 NUMBER OF SEQ ID NOS: 3
1 SOFTWARE: Microsoft Word 97 (IBM compatible)
1 SEQ ID NO 2
1 LENGTH: 801
1 TYPE: DNA
1 ORGANISM: Staphylococcus aureus

Query Match	Best Local Similarity	Score	DB	4;	Length	801;	
	Matches	Pred. No.	Mismatches	226;	Indels	Gaps	4;
2Y	56	AAATATAATTCTTATGAGGTGACCCGTACTCAGGAAATGTGAATCTTG	115				
Db	146	AAATAAAGAATTTGATGATATAATCATGATACGGTAACTCGTTAACATG	205				
2Y	116	ATCAACTTTATCACCATTAAATAATAATGTTCAGGCCA-----AATTATG	166				
Db	206	ATCAATTGCACTTGCATTGACTTGAATTAATCTATAAGGACACTAGTTAGG	265				
2Y	167	ATAAAATAAAAACTGAACTTAAGAACCAAGAGATGGCAACTTTATTAAGGAT	226				
Db	266	ATATGTTGAGTGAATTTAAACAAAGATTAGCTGATAAAACAAATAATACG	325				
2Y	227	TGATATTTATGGTGTGAGATAATTACATCTGTATTATGTTAAA-----	275				
Db	326	TAGATGTTGAGCTTAATGCTTATATCAATGTCATTCTGTTAAAACGATGATA	385				
2Y	276	-----TGGAGAAAGGGAGTGCACTGATGTTACGGGGGTAAACAAATCATG	319				
Db	386	TTAATTGCACTAACCTGACAAACGAAAAACTGTGATGGTGTGAACTGAC	445				
2Y	320	AAGGGAAATCATTGAAATTCTAAAAGATAATGCTGGTTAAAGTATGATGTT	379				
Db	446	ATGGAAACCAATTAGATATAATAGAACTTACTGTGGTAAATTGAGATGAAA	505				
2Y	380	AAAGCCATTCAATTGATATTGAAACAAATAAAANTGSTAACGCTCAGAAATT	439				
Db	506	ATTATATCCTTGACCGTACAAACTTAATAGAAAGGGACTGCTCAAAGAATT	565				
2Y	440	ATAAAAGTTGAAATAATCTTACAGATAATAAGCCTACTATATACTGACCTT	499				
Db	566	ACCTAACTCGTCACTATTGGTGAAAAATAAAACTCTPATGAATTAAACACT	625				
2Y	500	ATGAAACTGGATATATAAGTCTACACTTAAGATAAAAGAAGTTTGCTTGT	559				
Db	626	ATGAAACGGATATATAATTTATA---GAAATGAGATAGCTTGTGATGAA	682				
2Y	560	TCCCTGAAACCG----AATTACTCAATCTAAATACTTGTATATAAGATAATG	613				
Db	683	TGCTGACCGAGATAATTGACCATCTAAATTTAATGATGAACTGAAATA	742				
2Y	614	AAACGCTTGACTCAAACACAAGCCAAAATTGAACTCTAACAAACAAAG	663				

RESULT: 10
S-09-350-755A-2
Sequence 2, Application US/09350755A
Patent No. 6612640
GENERAL INFORMATION:
APPLICANT: United States Army Medical Research Institute of Infectious Diseases

RESULT 11
US-09-144-776B-9
; Sequence 9, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPARENTANT: Robert C. Murch

Mark A. Olson
Sina Bavari Superantigen
Vaccines

TITLE OF INVENTION: Bacterial Superantigen
SEQUENCES: 25

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris -Patent
Atty)

CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-SEP-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/882,431
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1388
TYPE: Nucleic Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-144-776B-9

Query Match 24.0%; Score 158.8; DB 4; Length 1388;
Best Local Similarity 58.3%; Pred. No. 7; e-28; Indels 45; Gaps 4;
Matches 379; Conservative 0; Mismatches 226;

QY 56 AAAATATAATTCTTTATGAGGTGACCCGTGTACTCACCGAAATCTGGTAATCTGGTG 115
DB 65 AAAATGAAAGTTTGTATGATGATAATCATGTATCAAGTAAACGTAAATCTAG 124

QY 116 ATCAACTTTATTCACCATTAAATAATAATGTTCAAGGGCCA-----AATATG 166
DB 125 ATCAATTGATGAACTTGTGACTTAACTTAACTAACTGTTAGGAATATG 184

QY 167 ATAATATAAAACTGAACTTAAGACCAAGAGATGCCACTTATAGATAAAACG 226
DB 185 ATAATGTTGAGTGAATTAAACAAAGATTAGCTGATAATAAACAGATAATAG 244

QY 227 TGTATATTATGGTGTGAGATAATTACACATCTGTATTATGTGAA----- 275
DB 245 TAGATGTTGGTGGCTAACTGCTTAAACAAACGATA 304

QY 276 -----TGCAAGAAAGGAGTGCATCTACGGGGTAACAAATATG 319
DB 305 TAATTGZCATCAAACGACAAACAAACTTATGTTAGGTGTTACTCGGACATA 364

QY 320 AGGGATCATTTAGAAATTCTAAAAGAGATGCTGTTAAAGTCAATCGTGTACCC 379
DB 365 ATGAAACCAATTAGATAATAAGATTACTGTTGGPATTGTGAGATGTA 424

QY 380 AAAGCTCATTTGATATGAAACAATAAAATGTAACTGCTGAAATTAGCT 439

Db 425 ATTATTATCTTTGAGCTAACACTAATAGAAAGGTGACTGCTCAAGBATTAGATT 484
Qy 440 ATAAAGTTAGAAAATATCTTACAGATAATAAGGAACTATATACTATGGACCTCTPAAT 499
Db 485 ACCTAACCTCGTAACTTGGTGRAMATAAAACTATGAATTAAACACTCGCCTT 544

Qy 500 ATGAAACTGGATAATAAGGTCTACCTAAGATAAGAAAGTTTGGTTGATTTT 559
Db 545 ATGAAAGGGATAATAATTATA---GAAATGAAATAATGATGACATGA 601

Qy 560 TCCGTGACCGA-----AATTACTCAATCTAAATGATGATAAGGTT 613
Db 602 TGCTGACCGAGATAATTGACCAATCTAAATGATGACATAATGACAATA 661

Qy 614 AACGCTGTGACTCAAACACAACCAATTGGACTTACCTAACAAAG 663
Db 662 AAATGGTGTAAAGATGAAATTGAGTTATCTACGACAAG 711

RESULT 12
US-09-144-776B-7
Sequence 7, Application US/09144776B
Patent No. 639932

GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen
SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris -Patient
Atty)

CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris -Patient
Atty)

ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712;
Best Local Similarity 58.3%; Pred. No. 7; e-28; Indels 45; Gaps 4;
Matches 379; Conservative 0; Mismatches 226;

QY 379 Query Match 24.0%; Score 158.8; DB 4; Length 1712;
Best Local Similarity 58.3%; Pred. No. 7; e-28; Indels 45; Gaps 4;
Matches 379; Conservative 0; Mismatches 226;

Qy 379 Qy 379

3.89 AAAATGAAACTTGTATGATAATTACGTAAATAAACGTTAAATCTATAG 4.48
 Db 3.89 AAAATGAAACTTGTATGATAATTACGTAAATAAACGTTAAATCTATAG 4.48
 Qy 11.6 ATCAACTTATCTCACCATTAAATATAATGTTCAAGGCCA-----AATTAG 1.66
 Db 4.49 ATCAAATTGACTTGTACTTAATCTTAAAGACACTAACTAAGGGATTAG 5.08
 Qy 16.7 ATAATTAAAACTGAACCTAAAGAAGATGGCAATTAACTTAAAGGATAAAAACG 2.26
 Db 5.09 ATAATGTTGAGTAAAGATTAAAGGATATACTGATAAAACAAAGATAACG 5.68
 Qy 22.7 TTGATATTATGGTAGAATTACCATCTGTATTATGTGAAA-----2.75
 Db 5.69 TAGATGTTGGCTTAAAGATTAAAGGATATACTGCTTTCTAAAAAACGAAATGATA 6.28
 Qy 27.6 -----TGCGAAAGGAGTGTGATPATCTACGGGGTACAATCATG 3.19
 Db 6.29 TTAATTGATCAAACCTGACAACGAAAACATTGATGTGGTAACTGGATA 6.88
 Qy 32.0 AAGGGATACATTGAAATTCTAAAGGATAGTCAATCGATGGTATCC 3.79
 Db 6.89 ATGAAACAAATTGATAATATGAGATTACTGTCGGTATTGAGATGTTAA 7.48
 Qy 38.0 AAAGCCTATCATTTGATGAAACAATAAAATGTAACCTCAAGAAATTAGACT 4.39
 Db 7.49 ATTATTATCTTTGACGAAACTAAAGAAAGGTGACTCTCAGAAATTAGTT 8.08
 Qy 4.40 ATAAGTGAACAAATPATCPACAGATAATAGCACTATACATGACCTCTAAAT 4.99
 Db 8.09 ACCTAACTCGTCACATTGTTGAAATAAAACTCATGAAATTACAACCTGCCCT 8.68
 Qy 50.0 ATGAAACTGATATAAGTTCACCTTAAAGAAGTTGGTTGGTTGATTTT 5.59
 Db 8.69 ATGAAACGGGATATAATTAAATTATA---GAAATGAGATAAGTTGGTATGACATA 9.25
 Qy 56.0 TCCCCTGAAACCGA-----AATTACTCACTAAATATCTTATGATATAAGGATAATG 6.13
 Db 9.26 TGCTGCAAGGAGATAATTGACCAATCTAAATATTGATGACAAATGACAATA 9.85
 Qy 61.4 AAACCTGACTCAACACAAGCCAAATCAAGGCTACCTAACACCAAG 6.63
 Db 9.86 AAATGGTCAAGGATCTAAAGATGTGAGATTTACCTTACGACAAG 10.35
 RESULT 1.3
 US-09-414-276-7
 Sequence 7, Application US/09414276
 i Patent No. 6392121
 i GENERAL INFORMATION:
 i APPLICANT: Mason, Hugh
 i APPLICANT: Palmer, Kenneth
 i APPLICANT: Heffron, Kathleen
 i APPLICANT: Mor, Tsafri
 i APPLICANT: Arntzen, Charles
 i TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
 i FILE REFERENCE: 4858/84453
 i CURRENT APPLICATION NUMBER: US/09/414,276
 i CURRENT FILING DATE: 1999-10-07
 i NUMBER OF SEQ ID NOS: 22
 i SOFTWARE: Patentin Ver. 2.0
 i SEQ ID NO 7
 i LENGTH: 815
 i TYPE: DNA
 i ORGANISM: bean yellow dwarf virus
 i FEATURE:
 i NAME/KEY: CDS
 i LOCATION: (3) ..(803)
 i US-09-414-276-7
 Query Match 16.9%; Score 112; DB 4; Length 815;
 Best Local Similarity 58.8%; Pred. No. 3.8e-17;
 Matches 234; Conservative 0; Mismatches 155; Indels 9; Gaps 2;

Qy 272 AAAATGCGAAAGGAGTGCATGTATCTACCGAGGGTAAACAATCATGAGGGATCATT 3.31
 Db 4.00 AACATGACGAGAAAGACTGCGTATGCTGACTGCTATGCGGTTGACTGAGGAAACRAAT 4.59
 Qy 3.32 TAGAAATTCTAAAGATAGTGTCAAAGTATCATGTTGATCCAAAGCCTATCAT 3.91
 Db 4.60 TGGAAATACTAGGGCATACTGTGAGGTGTTGAGATGTTAGAAACCTCCCTCTCTT 5.19
 Qy 3.92 TTGATATTGAAACATAAAATGTAAGTCAAGATTAGACTATAAGTTAGAA 4.51
 Db 5.20 TTGATGTCACAACTAACAGAAGGGTGTCTGCTCAAGGTTGACTACCTCTACTAGGC 5.79
 Qy 4.52 AATATCTTACAGATTTAAAGCACTATATACTAATGGCTTAAATGAAACTGGAT 5.11
 Db 5.80 ACTACTGGTGAAGAACAGAAAGCTTAAAGCTTAAACAGCCCTTAAGATGGAT 6.39
 Qy 5.12 ATATTAAGTTCATACCTAATGAAAGATTTGGTTGATTTTTCCTGACCCAG 5.71
 Db 6.40 ACATGAAGTCTATCAGCTTCTGGTATGACTGATCCTGGACCCAG 6.96
 Qy 5.72 -----ATTACTCATCTAAATCTATGATATAAGATAATGAAACGCTGTGACT 6.25
 Db 6.97 GAGAACAGTTGACCAATCTAAGTACCTCTGATGATGACAAAGATGGGACT 7.56
 Qy 6.26 CAAACACAAAGCCAAATTGAGTCTACCTTACAAACCAAG 6.63
 Db 7.57 CTAAAGTGTGAAGTTGGGTGACCTTACCCACCAAG 7.94
 RESULT 14
 US-09-14-776B-3
 Sequence 3, Application US/09144776B
 i Patent No. 639332
 i GENERAL INFORMATION:
 i APPLICANT: Robert G. Ulrich,
 i Mark A. Olson
 i Sina Bavari
 i TITLE OF INVENTION: Bacterial Superantigen
 i NUMBER OF SEQUENCES: 25
 i CORRESPONDENCE ADDRESS:
 i ADDRESSEE: Charles H. Harris
 i STREET: US Army MRMC -504 Scott Street
 i MCMR-JA (Charles H. Harris) Patent
 i Atty
 i CITY: FORT DETRICK
 i STATE: MARYLAND
 i COUNTRY: USA
 i ZIP: 21702-5012
 i COMPUTER READABLE FORM:
 i MEDIUM TYPE: FLOPPY DISK
 i COMPUTER: Apple Macintosh
 i OPERATING SYSTEM: Macintosh
 i SOFTWARE: Microsoft Word 7.5
 i CURRENT APPLICATION DATA:
 i APPLICATION NUMBER: US/09/144,776B
 i FILING DATE: 01-SEP-1998
 i CLASSIFICATION: <Unknown>
 i PRIORITY APPLICATION DATA:
 i APPLICATION NUMBER: 08/882,431
 i FILING DATE: <Unknown>
 i ATTORNEY/AGENT INFORMATION:
 i NAME: Charles H. Harris
 i REGISTRATION NUMBER: 34,616
 i REFERENCE/DOCKET NUMBER: <Unknown>
 i TELECOMMUNICATION INFORMATION:
 i TELEPHONE: (301) 619-2065
 i TELEFAX: (301) 619-7714
 i INFORMATION FOR SEQ ID NO: 3;
 i SEQUENCE CHARACTERISTICS:
 i LENGTH: 757
 i TYPE: Nucleic Acid
 i STRANDEDNESS: Unknown

;

;

TOPOLGY: Unknown

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-144-776B-3

Query Match 10.7%; Score 71; DB 4; Length 757;
Best Local Similarity 47.8%; Pred. No. 1e-07;
Matches 311; Conservative 0; Mismatches 325; Indels 15; Gaps 3;

;

US-09-350-755A-1

;

LENGTH: 757 ;
TYPE: DNA ;
ORGANISM: *Staphylococcus aureus*

Query Match 10.7%; Score 71; DB 4; Length 757;
Best Local Similarity 47.8%; Pred. No. 1e-07;
Matches 311; Conservative 0; Mismatches 325; Indels 15; Gaps 3;

;

US-09-350-755A-1

;

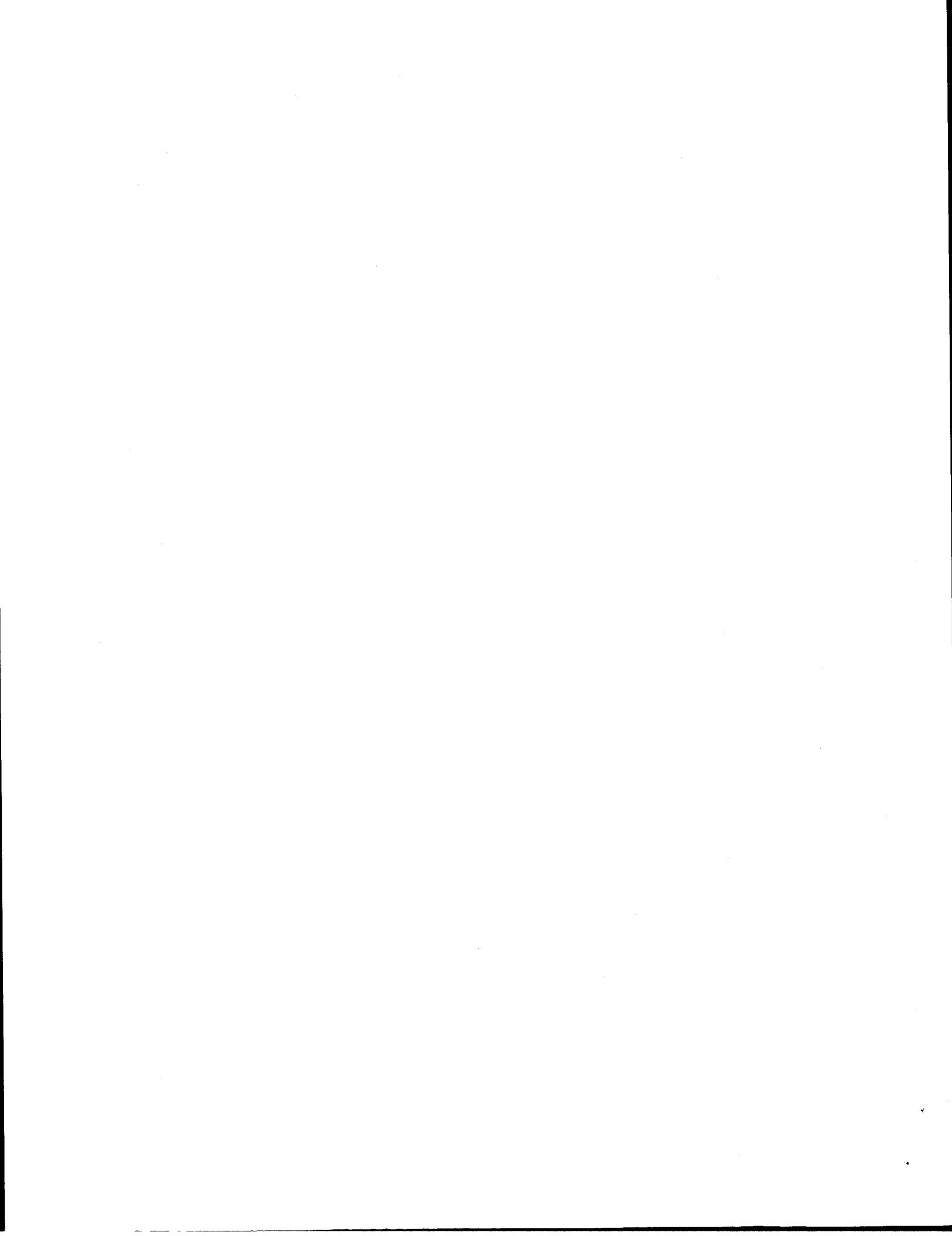
Match Number	Start Position	End Position	Sequence
QY	23	23	AACTTCAAGATTAGTTAGTTAGTTAGTTAAACCTTCAAATATAATTATTCCTTATGAGGTG 82
Db	49	49	AATTGGGGAAACGGCTTAGGCAATCTTAAACAACTCTATTAACTGAAAAGCTA 108
QY	83	83	ACCTCTTACTCTACGAGAAATGTCAAATCTGAACTTCTCACCATTAAAT 142
Db	109	109	AACTGAAAATAAGGAGTCAGTAAATTGAGCACACTATTTGTAAAGCT 168
QY	143	143	ATAATGTTTACGGCCAAATTATGATAAATTAAACTGAACTTAAAGAACAGATGG 202
Db	169	169	TTTTACAGATCATTCGGTATAACGATTATTAGTACGTTTGATTCRAAGGATRTG 228
QY	203	203	CAACTTATTAAAGGATAAAAGCTGATAATTATGGTGTAAATAATTACCTCTCTTT 262
Db	229	229	TGATAAAATATAAGGAAAAAGTAGTACCTGCTPATGGTGTATCAATG-- 286
QY	263	263	ATTATATGAAATGCGAAAGGCGTACATGAAATCATGAAAG 322
Db	287	287	-TGGGGGTTAACCCACAAACAGTTAACCAACAGTTGATGTTAGTGTGTTACATATA 345
QY	323	323	GGAAATCATTAGAAATTCCTAAAAGGAGTACGTCCTTAAGTGTAAATCGGTATCCAA 382
Db	346	346	ATAATGATTGACGCCGATCAATTATSGCTAACGGTAAACAAA 405
QY	383	383	GCCTATCATTTGA-----TATTGAAACAAATAAAATGGTAACTGCTCAGAAATTAG 436
Db	406	406	ATACAGTACCTTGGAAACGGTTAACAAAGAATAGGAAATGTAACCTGTTAGGTGG 465
QY	437	437	ACTATAAGTTAGAAAATATCTACAGATAATAGCAACTATAACATGGACCTCT- 495
Db	466	466	ATCTTCAGCAAGACGTTATTCAGGAAAAAATATAATTCTGATGTTTTG 525
QY	496	496	----AAATATGAAACTGGATATAAAGTTCATACCTPAGATAAAGGTTTTGGT 550
Db	526	526	ATGGAAAGGTTGGGGATTAATCTGTTACAGAACCTTCGGTAAATT 585
QY	551	551	TGATTATTTCCCTGAAACGAAATTACTCAAACTAAATATCTGATATAAAAGATA 610
Db	586	586	ACGGATTATTTGGTGTCAAGGAGCAGTAACTCAAACTATAAGGATATAAGAGATA 645
QY	611	611	ATGAAACGTTGACTCAAACAGCCAATGGAGTCACTTAACACACCA 661
Db	646	646	ATAAAACGATTAACTCTGAAAACATGGCATATTGATATAATTTATACAA 696

;

;

RESULT 15
US-09-350-755A-1
; Sequence 1, Application US/09350755A
; Patent No. 6632640
GENERAL INFORMATION:
; APPLICANT: United States Army Medical Research Institute of Infectious Diseases
; APPLICANT: Lee, John Scott
; APPLICANT: Pushko, Peter
; APPLICANT: Smith, Jonathan F.
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Vaccine Against *Staphylococcus* Intoxication
; FILE REFERENCE: Army-136
; CURRENT APPLICATION NUMBER: US/09/350,755A
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/032,416
; PRIORITY FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 97 (IBM compatible)
; SEQ ID NO 1

Search completed: September 3, 2004, 18:58:10
Job time : 82 secs



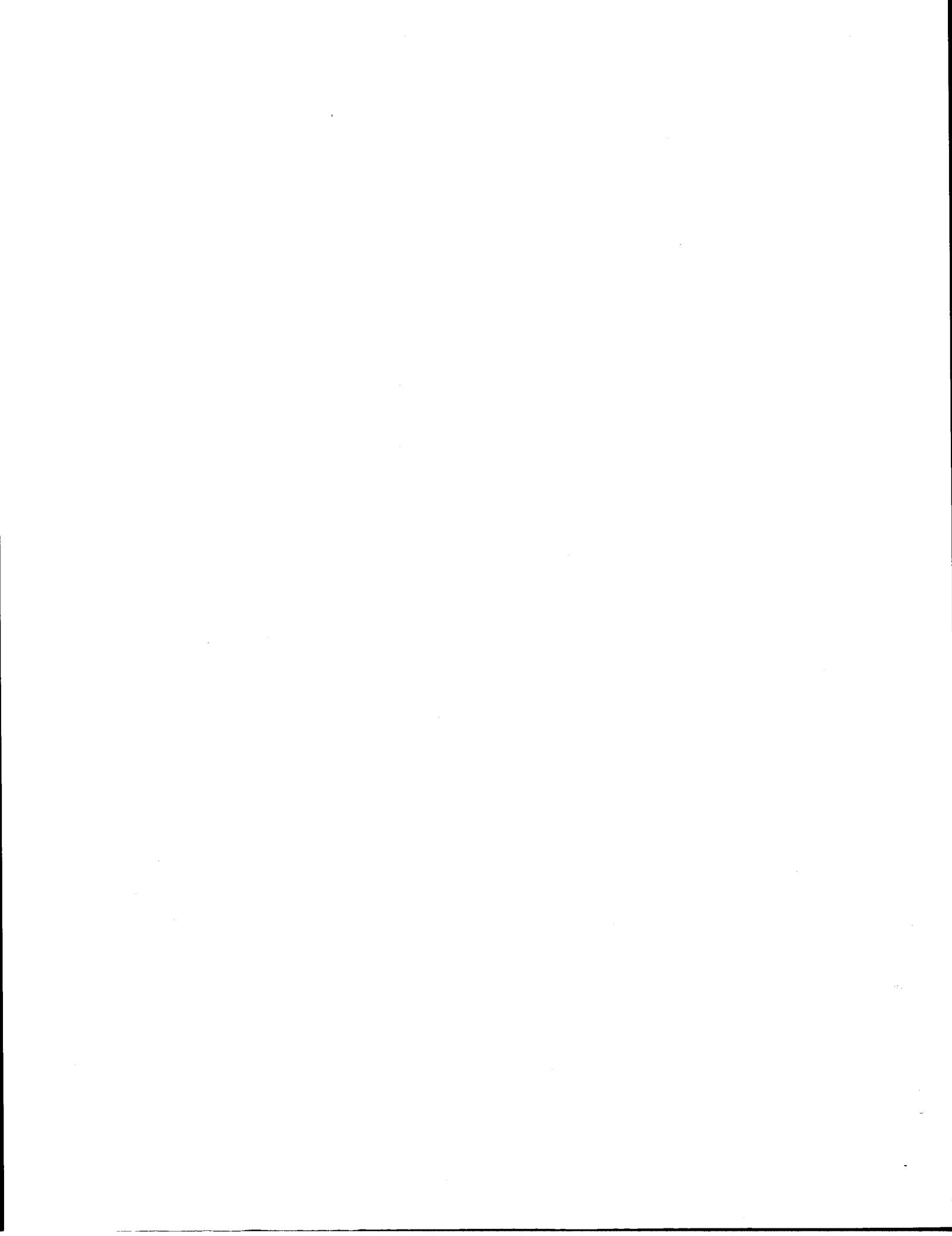
Db 739 TTTTTTACAAAAATAATTTPATGTTTATACTTAAATCAATATCT 680
 Qy 717 AATTAACTTAAATAGTTAGCTTTCATGTGTTGATATGGATGTTA 776
 Db 679 TAGATGTTTCTATAAGTAACTTAAAGGTTAGTTACTTACGTT 620
 Qy 777 TAACCTTAAATCTAGGGAAACCGAATATAATGGAAATTATGGAAAC 836
 Db 619 TTCTTTATGAAATTCCGTAATCTAACTGCATCAAGTATAGGGCTTGACAA 560
 Qy 837 ATAAATAGTGAAGAAAT 859
 Db 559 TCAATTATGTTGAGGAAAT 537

RESULT 2
 US-08-304-732B-25
 Sequence 25, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: OUELLETTE, Marc
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY NUMBER OF SEQUENCES: 134
 CORRESPONDENCE ADDRESS:
 ADDRESS: Quarles & Brady FORM:
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 35,433
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586-90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5000
 TELEFAX: (414) 277-5591
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5953 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Lactococcus lactis
 US-08-304-732B-35

Query Match 1.6%; Score 30; DB 1; Length 5953;
 Best Local Similarity 50.3%; Pred. No. 0.36; Gaps 1;
 Matches 97; Conservative 0; Mismatches 90; Indels 6; Gaps 1;
 Qy 609 TTTCATCCTTCACTTCAATTCTTAAAGATAAAATACATGTTTGTGA 668
 Db 257 TTATTCAAGCCACCACTAGCTTGGTAATTAATAGCTTTAACCTGCT 198
 Qy 669 TTATTAATAATTAATTATATAAGTTAATGTTTAAATAATPACATTATTCTA 728
 Db 197 TTCTCT-----TTTTTTATAAGTTAGGTGCTATTAGCTCTTACCTATGAG 144
 Qy 729 TTATATTTCTTATTTCTTCACTGTTAATTTAACTTACCTTTAA 768
 Best Local Similarity 59.2%; Pred. No. 0.05; Gaps 0;
 Matches 58; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 Qy 639 AGATAAAATPACATTGTTTGTATTATAATAATTAATTAATAGTTA 698
 Db 665 ATAAAAAAACATCTAGATGTTGTTTACCTAAACCACTAAATTATT 84
 Qy 699 TGTGTTTAAATACTATTTCTTCACTTATTTAGTTAATTTAGTTA 736
 Db 725 TTTGTAATTTAGATGTTTACCTGTTAATTTAACTTACCTAAATTATT 762

RESULT 4
 US-08-304-732B-31
 Sequence 31, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.

RESULT 3
 US-08-304-732B-35/c
 Sequence 35, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: OUELLETTE, Marc
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY NUMBER OF SEQUENCES: 134
 CORRESPONDENCE ADDRESS:
 ADDRESS: Quarles & Brady FORM:
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586-90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5000
 TELEFAX: (414) 277-5591
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5953 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Lactococcus lactis
 US-08-304-732B-35



APPLICANT: OUELIETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
 NUMBER OF SEQUENCES: 134
 COMPUTER READABLE FORM:
 ADDRESSER: Charles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 PUBLISH DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586-90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5591
 FAX: (414) 277-5000
 INFORMATION FOR SEQ ID NO: 31:
 LENGTH: 3754 base pairs
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid pairs
 STRANDEDNESS: double
 TOPOLOGY: linear
 ORIGINAL SOURCE: Lactococcus lactis
 US-08-304-732B-35

Query Match 1.5%; Score 28.6; DB 1; Length 5953;
 Best Local Similarity 50.8%; Pred. No. 0; Gaps 0;
 Matches 91; Conservative 0; Mismatches 84; Indels 4; Gaps 1;
 Sequence characteristics:
 Qy 697 ATGTTTTTAAATAATACATTATTCATTCTTACTTGTATTTCTGTTA 756
 Db 47 AATAAAATAAGAGAAATTCAATTCTTACTTATATAAAATTAGTTAAGTTAA 106
 Qy 757 ---GTATATGGTGTATGGTAATAACCTTTAAATCAGGGAAACCCAGATAAA 812
 RESULT 6
 US-08-304-732B-24

Sequence 24, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: OUELIETTE, Marc G.
 APPLICANT: ROY, Paul H.
 APPLICANT: BERGERON, Michel G.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
 NUMBER OF SEQUENCES: 134
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

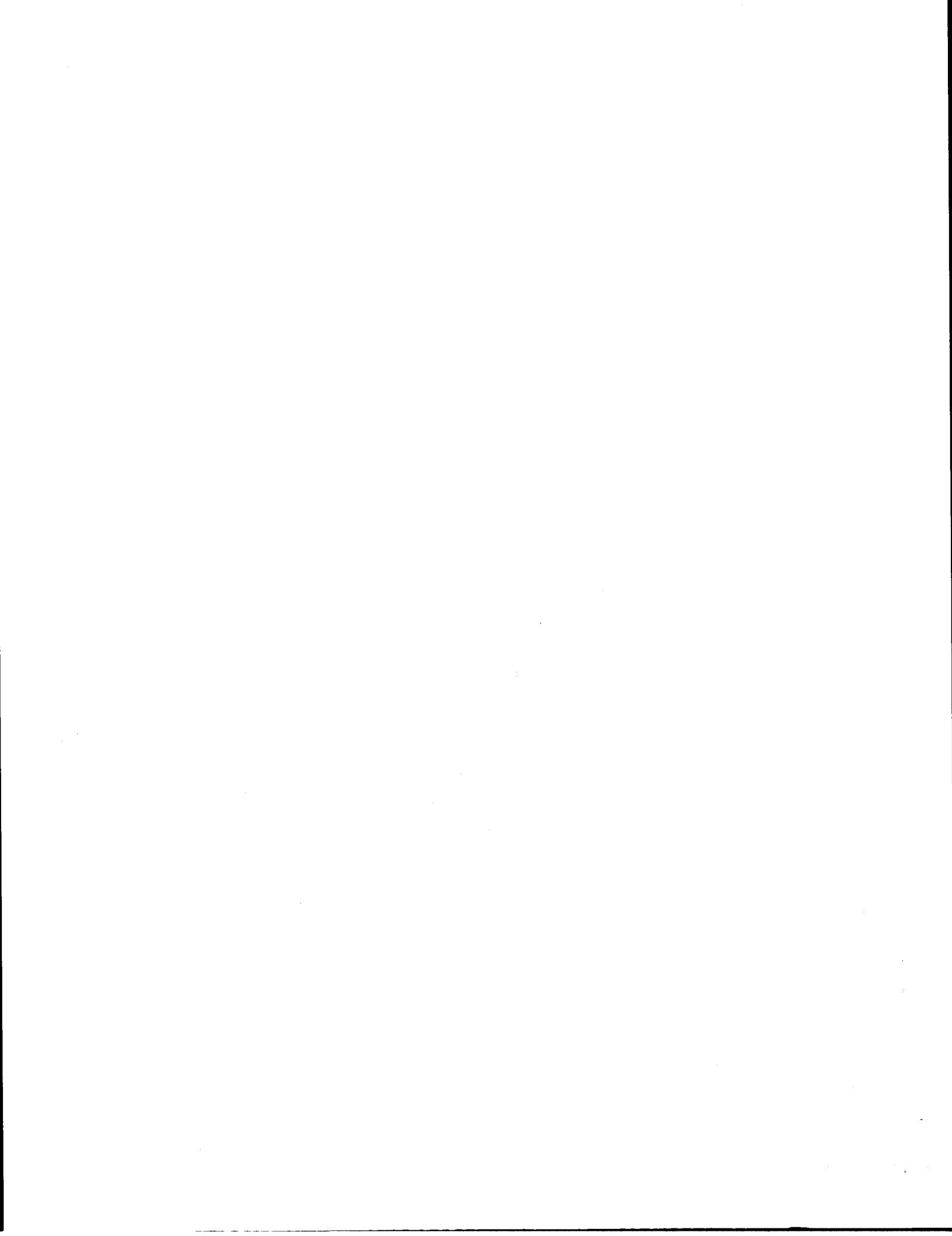
APPLICANT: OUELIETTE, Marc G.
 APPLICANT: ROY, Paul H.
 APPLICANT: BERGERON, Michel G.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
 NUMBER OF SEQUENCES: 134
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

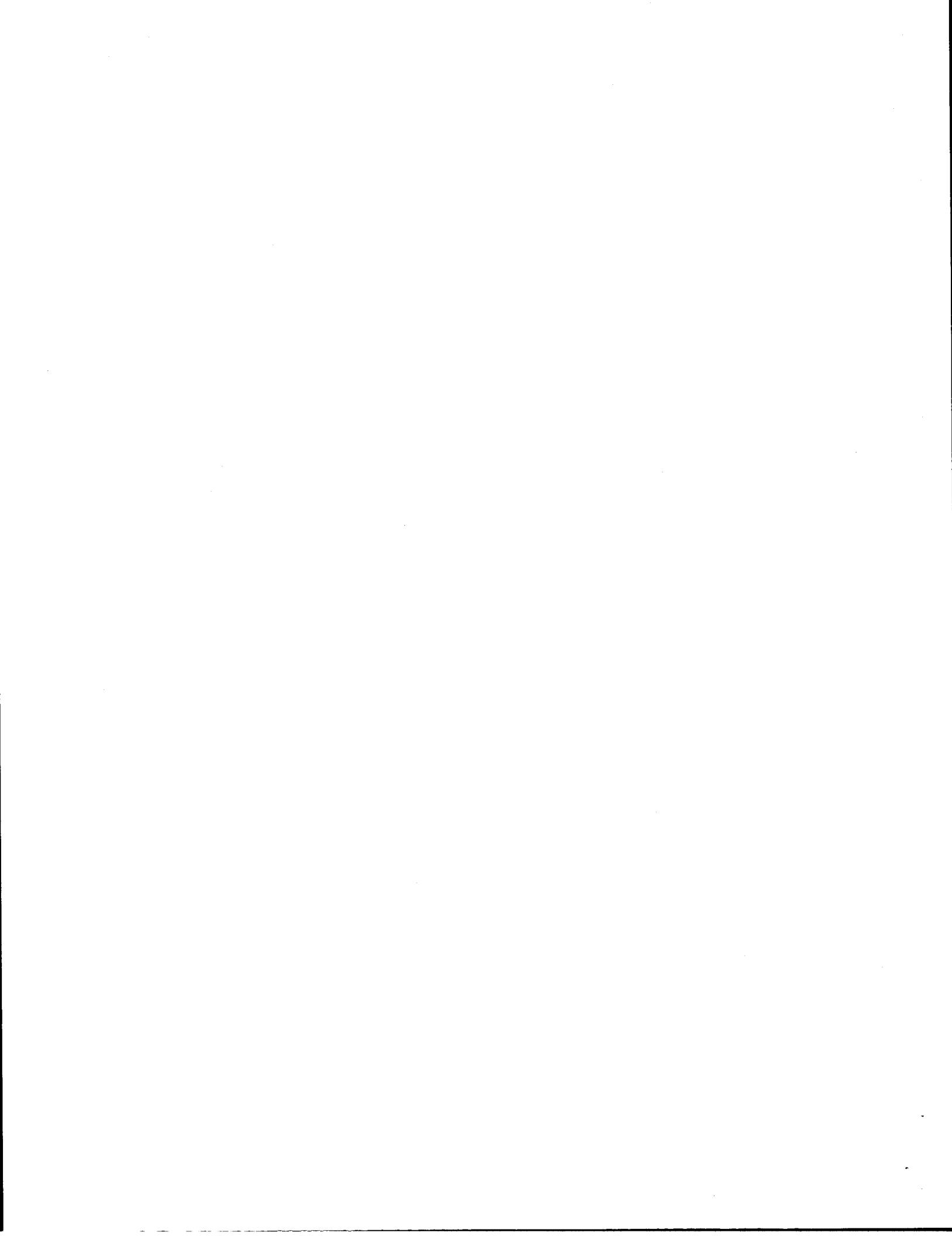
CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586-90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5591
 FAX: (414) 277-5000
 INFORMATION FOR SEQ ID NO: 35:
 LENGTH: 5953;
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid pairs
 STRANDEDNESS: double
 TOPOLOGY: linear
 ORIGINAL SOURCE: Lactococcus lactis
 US-08-304-732B-35

Query Match 1.5%; Score 28.6; DB 1; Length 5953;
 Best Local Similarity 50.8%; Pred. No. 0; Gaps 0;
 Matches 91; Conservative 0; Mismatches 84; Indels 4; Gaps 1;
 Sequence characteristics:
 Qy 697 ATGTTTTTAAATAATACATTATTCATTCTTACTTGTATTTCTGTTA 756
 Db 47 AATAAAATAAGAGAAATTCAATTCTTACTTATATAAAATTAGTTAAGTTAA 106
 Qy 757 ---GTATATGGTGTATGGTAATAACCTTTAAATCAGGGAAACCCAGATAAA 812
 RESULT 6
 US-08-304-732B-24

Sequence 24, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: OUELIETTE, Marc G.
 APPLICANT: ROY, Paul H.
 APPLICANT: BERGERON, Michel G.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
 NUMBER OF SEQUENCES: 134
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICANT: OUELIETTE, Marc G.
 APPLICANT: ROY, Paul H.
 APPLICANT: BERGERON, Michel G.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
 NUMBER OF SEQUENCES: 134
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:





MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE: Enterococcus faecalis
 US-08-304-732B-1

Query Match 1.4%; Score 26.4; DB 1; Length 1817;
 Best Local Similarity 51.7%; Pred. No. 1.7;
 Matches 60; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 1306 CATTGATTTGAAACAAATAAAAAATGGTAACTGTCAAGATTAGACTTAAAGTTA 1365
 Db 618 CAATGGGTAAGGAGGTTAAAAAAATTGCTTCGATTAATCCGAATCTAGATC 677

Qy 1366 GAAATATCTTACGATAATAGCACTATACTATGGACCTCTTATATGAA 1421
 Db 678 TTGTCCTTTAGCTATGGCAACCTGTAATAATGAGGGCAATTTATATAA 733

RESULT 9
 US-08-304-732B-15 Application US/08304732B

GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY

TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY

TITLE OF INVENTION: LABORATORY

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 850586.90012
 FILING DATE: 12-SEP-1994

TELECOMMUNICATION INFORMATION:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35.433
 TELEPHONE: (414) 277-5591
 TELEFAX: (414) 277-5000
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9100 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLogy: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Haemophilus influenzae

US-08-304-732B-27

Query Match 1.4%; Score 25.4; DB 1; Length 9100;
 Best Local Similarity 49.6%; Pred. No. 2.8;
 Matches 65; Mismatches 66; Indels 0; Gaps 0;

Qy 560 AATATACCCCTTATCATCGCTTCAATCTATATACATCTATACATTTCTCC 619
 Db 8079 AATATACTGCTTATCGCTTCTGGCTTCTGGCTTATPAGCCTCGGCCAGCCCC 8020

Db 620 TACCTATTTATGTAAGAATATAAAATTAATCTATTGTTTTTGTTATTTTATAAA 679
 Db 8019 ACATTTGAACTTCCTCCACCTTAATTTGCAACAATTGAGATTCTAGTGTAG 7960

Qy 680 AATTTATTAATA 690
 Db 7959 AACGAGTAGTA 7949

RESULT 11
 US-08-304-732B-26

US-08-304-732B-15 Application US/08304732B

GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY

TITLE OF INVENTION: OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY

TITLE OF INVENTION: LABORATORY

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 850586.90012
 FILING DATE: 12-SEP-1994

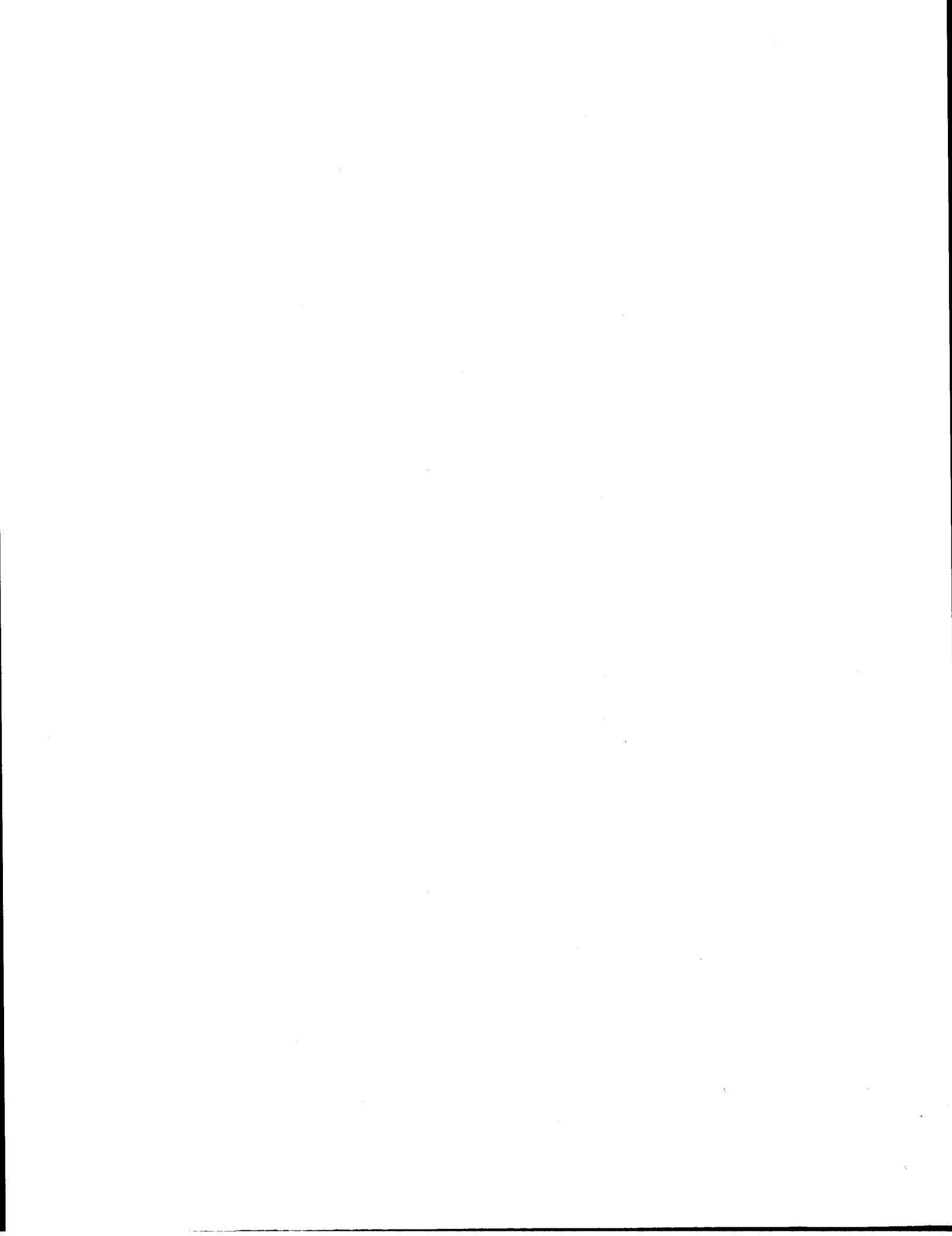
TELECOMMUNICATION INFORMATION:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35.433
 TELEPHONE: (414) 277-5591
 TELEFAX: (414) 277-5000
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9100 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLogy: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Proteus mirabilis

US-08-304-732B-15

Query Match 1.4%; Score 25.4; DB 1; Length 1346;
 Best Local Similarity 48.9%; Pred. No. 2.7;
 Matches 68; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 1314 ATCATTGATTTGAAACATAAATGTTACTGTCAAGATTAGCATATAAGT 1363
 Db 13 ATCAATCTTAAGAATTTTATTAATCTGATACTATGATACTATGATACTAT 72

Qy 1364 TAGAAATATCTACAGATATAAGCAACTATACATAATGACCTCTAAATGAAAC 1423



Sequence 26, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY

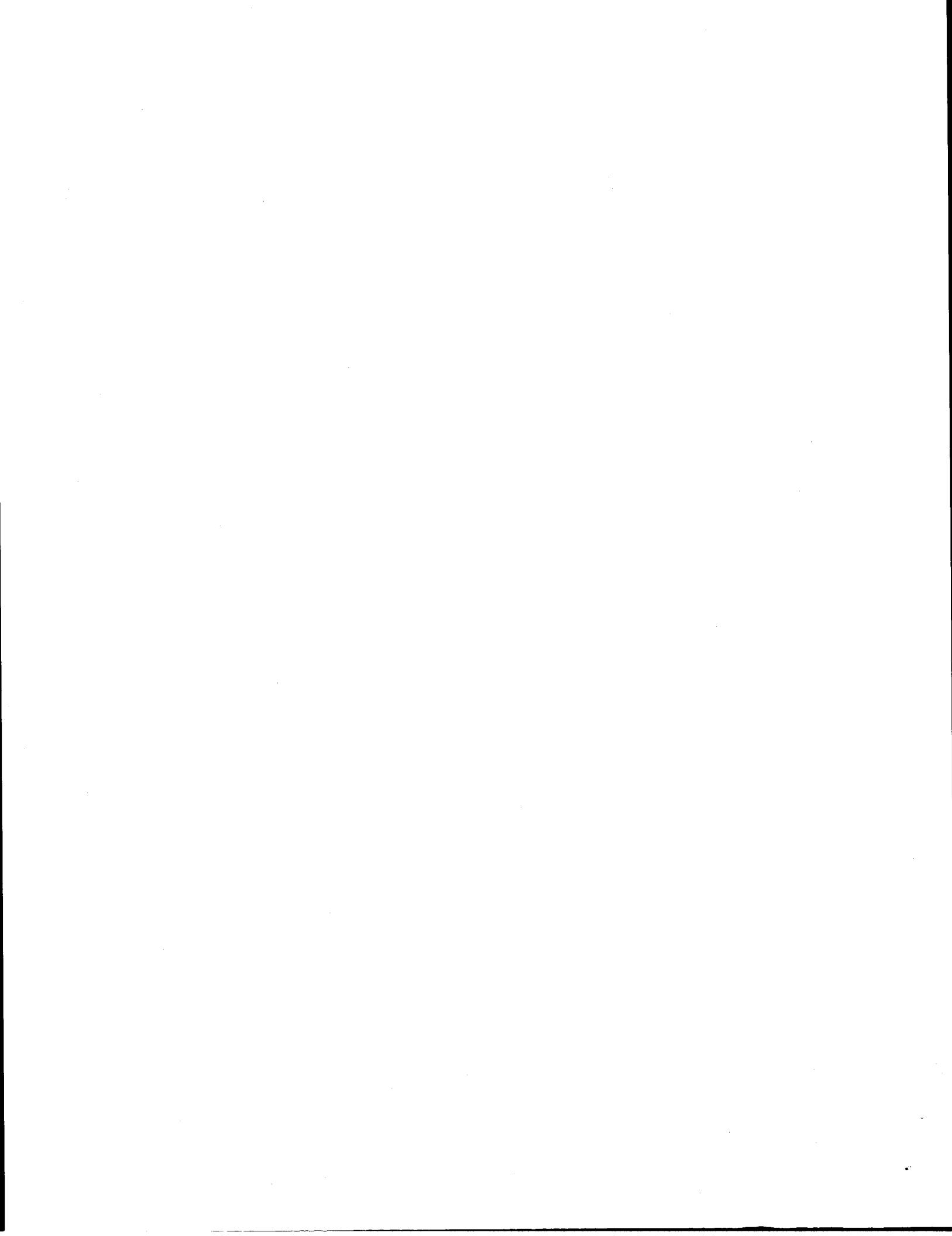
TITLE OF INVENTION: NUMBER OF SEQUENCES: 134
 TITLE OF INVENTION: LABORATORY
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.

US-08-304-732B-15/C
 Sequence 15, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY

TITLE OF INVENTION: NUMBER OF SEQUENCES: 134
 TITLE OF INVENTION: LABORATORY
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.

US-08-304-732B-15/C
 Sequence 15, Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY

TITLE OF INVENTION: NUMBER OF SEQUENCES: 134
 TITLE OF INVENTION: LABORATORY
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.



REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586.90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5000
 TELEFAX: (414) 277-5591
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2275 base pairs
 TYPE: nucleic acid
 STRANDBNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecalis
 US-08-304-732B-2

Query Match 1.34; Score 23.2; DB 1; Length 2275;
 Best Local Similarity 46.8%; Pred. No. 7-3; Indels 0; Gaps 0;
 Matches 73; Conservative 0; Mismatches 83;
 Qy 450 TCTCCACTCTCTACGGCAAACTTCATCATTCTCACTTTTCGTGTAACACA 509
 Db 1339 TCTTATGTTGTTGTTGAACTTCGAAATCCGTCACAGCGCATACCGAACATCCAT 1280
 Qy 510 TAATCATAATATCTTCCTTTACGGCTATCGTACTCTGCACTAAATATAACCC 569
 Db 1279 TGTCAGATAAGCTGGTTTCATAATATATGCCACCTCTCTGTAATAAGGTGAA 1220
 Qy 570 TTATCAGTCCTCTTAACTCATATATAAC 605
 Db 1219 CCACCAATATTTACAGGATAATCCAGC 1184

RESULT 14

US-08-304-732B-1/C

Sequence 1. Application US/08304732B
 GENERAL INFORMATION
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
 TITLE OF INVENTION: NUMBER OF SEQUENCES: 134
 ADDRESS: Quarles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586-90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5000
 TELEFAX: (414) 277-5591
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1817 base pairs
 TYPE: nucleic acid
 STRANDBNESS: double
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1817 base pairs
 TYPE: nucleic acid
 STRANDBNESS: double

TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecalis
 US-08-304-732B-1

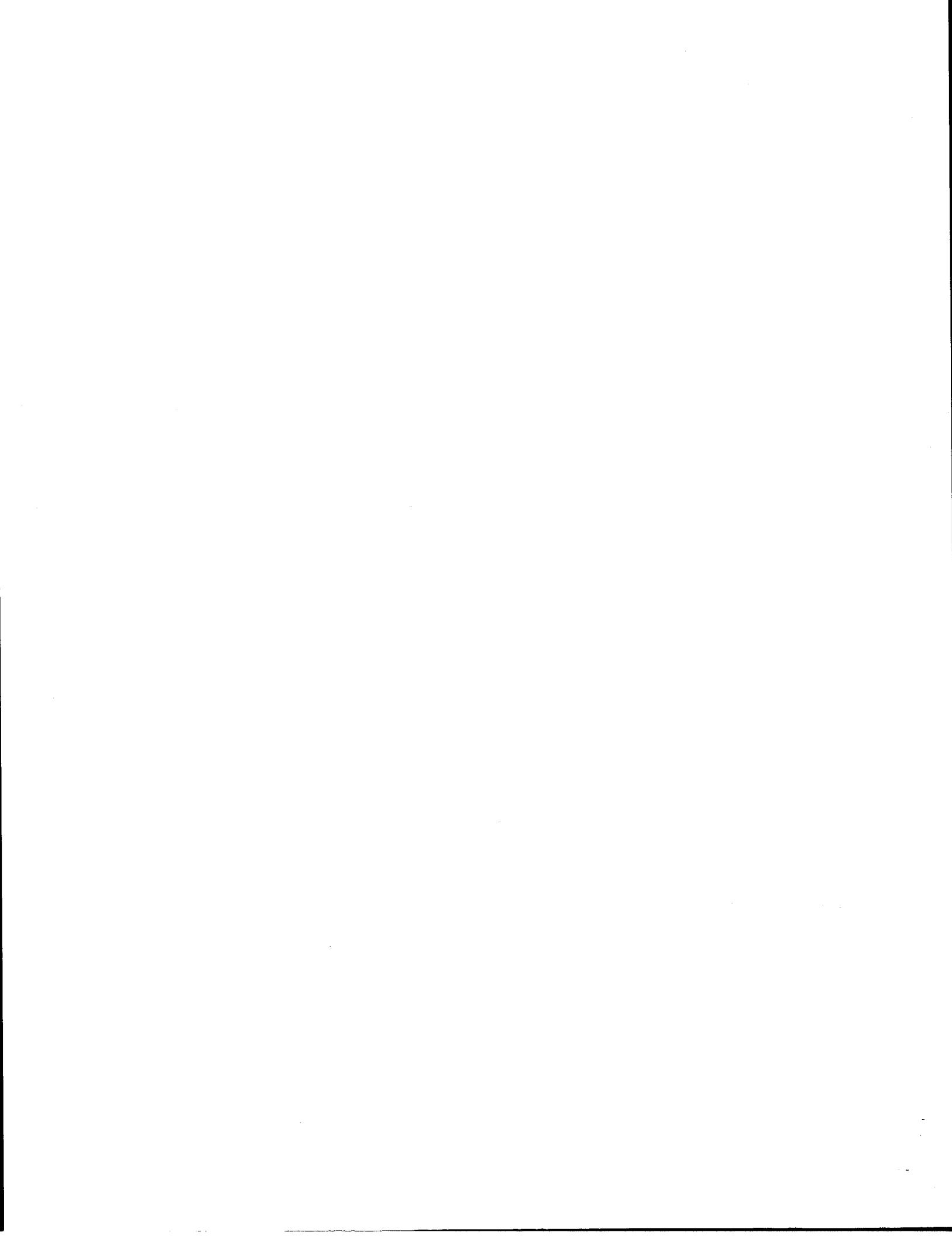
Query Match 1.2%; Score 22.6; DB 1; Length 1817;
 Best Local Similarity 45.7%; Pred. No. 9-5; Indels 0; Gaps 0;
 Matches 79; Conservative 0; Mismatches 94;
 Qy 1009 CTCAGGAGATGCAATTCTGATCAACTTATTCCTCCATTAAATATAATGTTT 1068
 Db 1102 CCCTGATCATCATCTGTTGGAATGATGTTCATATGTTTCACAAATT 1043
 Qy 1069 CAGGGCAAATTGTATAAATTAAGTAAACTGAACTTAAAGCTAGGCACITTT 1128
 Db 1042 TCCATGCTATAGCGGTATAGCATCTGTTGAAATTTACCTCTGTTGAT 983
 Qy 1129 TTAGGATAAAACGTTGATAATTTAGTTGAAATTTACCTCTGTTGAT 1181
 Db 982 AATAGATATTATTTGCCATCRACTGATGTAACCCGTGTAT 930

RESULT 15

US-08-304-732B-26/c

Sequence 26. Application US/08304732B
 GENERAL INFORMATION:
 APPLICANT: BERGERON, Michel G.
 APPLICANT: OUELLETTE, Marc
 APPLICANT: ROY, Paul H.
 TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIA FROM URINARY OR ANY OTHER BIOLOGICAL SAMPLES IN THE ROUTINE MICROBIOLOGY
 TITLE OF INVENTION: NUMBER OF SEQUENCES: 134
 CORRESPONDENCE ADDRESS:
 ADDRESS: Quarles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/304,732B
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 850586-90012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5000
 TELEFAX: (414) 277-5591
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1598 base pairs
 TYPE: nucleic acid
 STRANDBNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Haemophilus influenzae
 US-08-304-732B-26

Query Match 1.2%; Score 22.4; DB 1; Length 1598;
 Best Local Similarity 52.1%; Pred. No. 10;
 Matches 50; Conservative 0; Mismatches 46; Indels 0; Gaps 0;



Wed May 12 06:49:18 2004

align12_304732

Page 8

Qr 562 TATAACCCCTATCAATGCCCTCTTAACTCATCTTATATAACATACTTCCATCCTCCPA 621
Db 371 TATGCCCTCATCCATCTTGTATTATCTGAGCTTAAGGTTACATACCCATT 312
Qr 622 CCTATCPATTCGTAAAGATAAAAATAACTATGTT 657
Db 311 CATAATTCTCTAGAATCTATAAACGCCCTGT 276

Search completed: May 11, 2004, 16:57:10
Job time : 60 secs

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OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 17:12:26 ; Search time 373 seconds

Perfect score: US-10-625-221-12_COPY_918_1580
 Sequence: 663 1 caacaagacccgatccaag.....aatgtctacctaaacaacaaag 663

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04-*

1: geneseqn1980s;*
 2: geneseqn1990s;*
 3: geneseqn2000s;*
 4: geneseqn2001as;*
 5: geneseqn001bs;*
 6: geneseqn002as;*
 7: genes_qn2003as;*
 8: geneseqn003bs;*
 9: geneseqn003cs;*
 10: geneseqn2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	663	100.0	1851	2	AAT51716	Aatt1716 Streptococcus pyogenes
2	663	100.0	1851	2	AAV41593	Aav41593 Streptococcus pyogenes
3	661.4	99.8	1837	4	AHH01002	Aah01002 Unidentif. streptococcal species
4	661.4	99.8	1837	2	AAT28540	Aat28540 Streptococcus pyogenes
5	661.4	99.8	1837	4	ABA76857	ABA76857 Streptococcus pyogenes
6	658.2	99.3	1837	3	AAZ51112	AAZ51112 Streptococcus pyogenes
7	658.2	99.3	1837	6	ABN84229	ABN84229 Streptococcus pyogenes
8	658.2	99.3	1837	7	ACA61184	ACA61184 Streptococcus pyogenes
9	656.6	99.0	1837	8	AAD56771	Aad56771 Streptococcus pyogenes
10	656.6	99.0	1837	8	ACD28901	ACD28901 Streptococcus pyogenes
11	651.8	98.3	1419	8	ACD28908	ACD28908 Streptococcus pyogenes
12	651.8	98.3	1419	8	AAD56778	AAD56778 Streptococcus pyogenes
13	582.6	87.9	1031	7	ACA64700	ACA64700 Streptococcus pyogenes
14	167.4	25.2	1095	7	ACA64696	ACA64696 Streptococcus pyogenes
15	166.8	25.2	773	2	AAT45698	Aat45698 Streptococcus pyogenes
16	166.8	25.2	801	7	ACA64688	ACA64688 Streptococcus pyogenes
17	166.8	25.2	886	7	ACA64689	ACA64689 Streptococcus pyogenes
18	166.8	25.2	1712	3	Aaz51107	Aaz51107 Streptococcus pyogenes
19	166.8	25.2	1712	6	ABN84224	ABN84224 Streptococcus pyogenes
20	166.8	25.2	1712	7	ACA61179	ACA61179 Streptococcus pyogenes
21	166.8	25.2	1712	7	ACA64695	ACA64695 Streptococcus pyogenes
22	166.8	25.2	1712	8	ACD28896	ACD28896 Streptococcus pyogenes
23	166.8	25.2	1712	8	AAD56766	AAD56766 Streptococcus pyogenes

24	164.2	24.8	1095	3	AAZ51111	AAZ51111 Staphylococcus aureus
25	164.2	24.8	1095	6	ABN84228	ABN84228 Staphylococcus aureus
					Aca61183	Aca61183 DNA encod.
					Acd28900	Acd28900 S. aureus
					Aad56770	Aad56770 Staphylococcus aureus
					Aah74983	Aah74983 Nucleotid
					Aazz4835	Aazz4835 Mutant SE
					Aaz45334	Aaz45334 Mutant SE
					Aaz51109	Aaz51109 Mutant SE
					Abn84226	Abn84226 Staphylococcus aureus
					Aca61111	Aca61111 DNA encod.
					Acd28898	Acd28898 S. aureus
					Aad56768	Aad56768 DNA #4 re
					Aaa09240	Aaa09240 Plant-opt
					Aca64697	Aca64697 S. aureus
					Aca64694	Aca64694 S. aureus
					Add44369	Add44369 Staphylococcus aureus

ALIGNMENTS

RESULT 1
 AAT51716
 ID AAT51716 standard; DNA; 1851 BP.
 XX
 AC AAT51716;
 XX
 DT 04-NOV-1997 (first entry)
 XX
 DE Streptococcus pyogenes Streptococcal toxin A DNA.
 XX
 KW Streptococcal toxin A; SPE-A; non-lethal; mutant; production; vaccine;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
 KW hypertension; group A streptococcal infection; myositis; fascitis;
 KW liver damage; T cell; lymphoma; ovarian; uterine; ss.
 XX
 OS Streptococcus pyogenes.

XX
 Key Location/Qualifiers
 FH CDS 828..1583
 FT FT /*tag= a
 FT sig_peptide 828..917
 FT mat_peptide FT /*tag= b
 FT product= "Streptococcal_toxin_A"
 XX
 PN WO940930-A1.
 XX
 PD 19-DEC-1996.
 XX
 PR 07-JUN-1996; 96WO-US010252.
 XX
 PR 07-JUN-1995; 95US - 00480261.
 XX
 PA (M-TNU) UNIV MINNESOTA.
 XX
 PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
 XX
 DR WPI; 1997-09936/09.
 PR P-PDB; AAW12097.
 XX
 PT Mutant SPE-A toxin with at least one amino acid change is substantially
 non-lethal - used in vaccine composition for treatment of cancer and
 streptococcal toxic shock syndrome etc.

S Disclosure; Page 77-79; 102pp; English.

X The present sequence encodes *Streptococcus pyogenes* Streptococcal toxin A (SPE-A), from which a non-lethal mutant SPE-A, comprising at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells.

X	Sequence	1851 BP;	635 A;	326 C;	248 G;	642 T;	0 U;	0 Other;
Query Match	100.0%;	Score 663;	DB 2;	Length 1851;				
Best Local Similarity	100.0%;	Pred. No. 1e-120;						
Matches	663;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0			
Y	1 CAACAGAACCCGATCCAAGGCCAACCTCACAGATCTAGTTAGTAAAAACCTTCATAAAT 60							
b	918 CAACAGAACCCGATCCAAGGCCAACCTCACAGATCTAGTTAGTAAAAACCTTCATAAAT 977							
Y	61 ATATATTTCTTTATGGGTGACCCCTGTTACTCAGAGAATGTGAAATCTGTTGATCAA 120							
b	978 ATATATTTCTTTATGGGTGACCCCTGTTACTCAGAGAATGTGAAATCTGTTGATCAA 103							
Y	121 CTTTATCTCACATTAAATATAATGTTTCAGGGCCAATTAGATAAAATTAAACT 180							
b	1038 CTTTATCTCACATTAAATATAATGTTTCAGGGCCAATTAGATAAAATTAAACT 109							
Y	181 GAACTTAAAGAACCAAGAGATGGCAACTTTATTAGGATAAAAACCGTTGATATTATGGT 240							
b	1098 GAACTTAAAGAACCAAGAGATGGCAACTTTATTAGGATAAAAACCGTTGATATTATGGT 115							
Y	241 GTAGAAATTACATCTCTGTATTATGTGAAATACTGAAAGGAGTGATGATATCTAC 300							
b	1158 GTAGAAATTACATCTCTGTATTATGTGAAATACTGAAAGGAGTGATGATCTAC 121							
Y	3 01 GGAGGGTTAACAAATCATGAAGGGAAATTAGAAATTCCTAAGAAGATAGTCGTTAA 3 60							
b	1218 GGAGGGTTAACAAATCATGAAGGGAACTTACGAAATTCTAACAAAGATAGTCGTTAA 127							
Y	361 GATCATCGATGGTATCCAAAGCTATCATTTGATATTGAAACAAATAAAATGGTA 4 20							
b	1278 GATCATCGATGGTATCCAAAGCTATCATTTGATATTGAAACAAATAAAATGGTA 1 3 3							
Y	4 21 ACTGCTAAGAATTAGCTTAAAGCTGAAATATCTTACAGATAATAGGAACTTAT 4 80							
b	1338 ACTGCTAAGAATTAGCTTAAAGCTTACAGATAATAGGAACTTAT 13 9							
Y	4 81 ACTATGGACCTCTCAATATGAACTGATATAAAGGTCAACCTAAGGATAAANGAA 5 4 0							
b	1398 ACTATGGACCTCTCAATATGAACTGATATAAAGGTCAACCTAAGGATAAANGAA 14 5							
Y	541 AGTTTTGGTTGATTTTTCCTGAACCGAGATTACTCAACTTAATAATCTATGATA 6 0 0							
b	1458 AGTTTTGGTTGATTTTCCTGAACCGAGATTACTCAACTTAATAATCTATGATA 15 1							
Y	6 0 1 TATAAGATAATGAAACCGCTTACTCAACAGCCAAATTGAAAGCTACCTAACACC 6 6 0							
b	1518 TATAAGATAATGAAACCGCTTACTCAACAGCCAAATTGAAAGCTACCTAACACC 15 7							
Y	661 AAG 663							
b	1578 AAG 1580							

RESULT 2
AAV41593

Qy 241 GTAGAATAATTACATCTCGTATTATGTGAAATGCGAGAAAGGAGTCATGTATCTAC 300
 Db 1158 GTAGAATAATTACATCTCGTATTATGTGAAATGCGAGAAAGGAGTCATGTATCTAC 1217
 Qy 301 GAGGGGTAACTAACATTAGAAATTCCTAAAGATGTCGTTAA 360
 Db 1218 GAGGGGTAACTAACATTAGAAATTCCTAAAGATGTCGTTAA 1227
 Qy 361 GTATCATCGATGGTATCAAAGCCTATCAAGCTTAAAGATGTCGTTAA 1337
 Db 1278 GTATCATCGATGGTATCAAAGCCTATCAAGCTTAAAGATGTCGTTAA 1337
 Qy 421 ACTGCTAAGGATTAGCTATAAGTTGAAATACTTACAGATAAACCTATA 480
 Db 1338 ACTGCTAAGGATTAGCTATAAGTTGAAATACTTACAGATAAACCTATA 1397
 Qy 481 ACTAATGGACCTTCTAAATATGAAACTGATATAAAAGTCATACCTAGAAATAAAAGAA 540
 Db 1398 ACTAATGGACCTTCTAAATATGAAACTGATATAAAAGTCATACCTAGAAATAAAAGAA 1457
 Qy 541 AGTTTTTGTTGATTTCCTGAACTCAATTACTCAATTCTATCTATGATA 600
 Db 1458 AGTTTTTGTTGATTTCCTGAACTCAATTACTCAATTCTATCTATGATA 1517
 Qy 601 TATAAGATTAATGAAACAGCTGACTCAACACAAGGCAAAATTGAAAGTCATCTAACACC 660
 Db 1518 TATAAGATTAATGAAACAGCTGACTCAACACAAGGCAAAATTGAAAGTCATCTAACACC 1577
 Qy 661 AAG 663
 Db 1578 AAG 1580

RESULT 3
 AAH01002
 ID AAH01002 standard; DNA; 756 BP.
 XX
 AC AAH01002;
 XX DT 24-JUL-2001 (first entry)
 XX DE Unidentified nucleotide sequence SEQ ID NO:993.
 XX Species specific; genus specific; family specific; probe; detection;
 KW identification; algal; archaeal; bacterial; fungal; parasitical;
 KW microorganism; diagnosis; translation elongation factor tu; toxin;
 KW translation elongation factor G; RecA recombinase; resistance;
 KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KW primer; ds.
 XX OS Unidentified.
 XX PN WO200121604-A2.
 XX PR 28-SEP-2000; 2000000-CAD01150.
 XX PR 28-SEP-1999; 29-A-022-83458.
 XX PR 19-MAY-2000; 200000A-02307010.
 XX PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX DR Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX WPI; 2001-245006/25.

Disclosure: Page 957; 1580pp; English.

PS xx
 CC The present invention describes a method for generating a repertoire of nucleic acids of tuf, ftsY, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacteriaceae group, Escherichia coli, Pseudomonas group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results are determined in an hour and improved accuracy is also achieved. AAH00010 to AAH02304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.

SQ Sequence 756 BP; 297 A; 110 C; 118 G; 231 T; 0 U; 0 Other;
 Query Match 99.8%; Score 661.4; DB 4; Length 756;
 Best Local Similarity 99.8%; Pred. No. 2e-120;
 Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 CAACAGAGCCCCGATCCAGGCCAACCTCACAGATCTAGTTGTTAAAGACCTTCATAAT 60
Db	91 CAACAGAGCCCCGATCCAGGCCAACCTCACAGATCTAGTTGTTAAAGACCTTCATAAT 150
Qy	61 ATATTTTCTTCTTATGAGGTGACCTGTACTACAGAAATGGAATTTGTGATCAA 120
Db	151 ATATTTTCTTCTTATGAGGTGACCTGTACTACAGAAATGGAATTTGTGATCAA 210
Qy	121 CTTTATCTACCATTTAAATATAATGTTGTTCAGGCCAAATTATGATAAATTAAAAGCT 180
Db	211 CTTTATCTACCATTTAAATATAATGTTGTTCAGGCCAAATTATGATAAATTAAAAGCT 270
Qy	181 GAACTTAAGGACCAAGAGATGGCAACCTTTATTAAGGGATAAAACGTGATATTATGCT 240
Db	271 GAACTTAAGGACCAAGAGATGGCAACCTTTATTAAGGGATAAAACGTGATATTATGCT 330
Qy	241 GTAGAAATTACCATCTCTGTTATTATGTGAAATGAGAAGGAGTCGATGATCTAC 300
Db	331 GTAGAAATTACCATCTCTGTTATTATGTGAAATGAGAAGGAGTCGATGATCTAC 390
Qy	301 GGAGGGTTAACAAATCATGAAGGGATCATTTGAAATTCCTAAAGATAGTCGTTAA 360
Db	391 GGAGGGTTAACAAATCATGAAGGGATCATTTGAAATTCCTAAAGATAGTCGTTAA 450
Qy	361 GTATCAATCTGATGTTATCCTGTTATGTTATGTTATGTTATGTTATGTTATGTTA 420
Db	451 GTATCAATCTGATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTA 510
Qy	421 ACTGCTCAAGAAATTGAGCTATAGAGTAACTTCTGATATAGAACTATAGAACTAT 480
Db	511 ACTGCTCAAGAAATTGAGCTATAGAGTAACTTCTGATATAGAACTATAGAACTAT 570
Qy	481 ACTAATGGACCTCTAAATGAACTTCTGATATAAAGTCTGATATAAAGTCTGATATAAAGAA 540
Db	571 ACTAATGGACCTCTAAATGAACTTCTGATATAAAGTCTGATATAAAGTCTGATATAAAGAA 630
Qy	541 AGTTTGCTGTTGATTTTCCCTGAAACGAAATTACTCATCTAAATCTTGTATAAGATAAGAA 600
Db	631 AGTTTGCTGTTGATTTTCCCTGAAACGAAATTACTCATCTAAATCTTGTATAAGATAAGAA 690

CC resistance to beta-lactam antibiotics		XX	
Sequence 1837 BP; 631 A; 318 C; 248 G		SQ	
QY	1	CAACAA\$ACCCCGATCCAAGGCCAACTTC	Score 66%
DB	904	CAACAA\$GCCGATCCAAGGCCAACTTC	Best Local Similarity 99.8%; Predicted; Mismatches 662; Conservative 0;
QY	61	AATATTTCTTATGAGGTGACCCGTG	
DB	964	AATATTTCTTATGAGGTGACCCGTG	
QY	121	CTTTATCTACCATTATAATATATG	
DB	1024	CTTTATCTGATTATAATATATG	
QY	181	GAACTTAGAACCAAGGAGATGGCAACTT	
DB	1084	GAACTTAGAACCAAGGAGATGGCAACTT	
QY	241	G\$GAAATTACCATCTGTATTATAT	
DB	1144	GTA\$AATTACCATCTGTATTATAT	
QY	301	GGACGGGTAAACAAATCATGAAGGAATC	
DB	1204	GGGGGG\$AACAAATCATGAAGGAATC	
QY	361	GTA\$CAATCGATGGTACAAAGGCCPAT	
DB	1264	GTA\$CAATCGATGGTACAAAGGCCPAT	
QY	421	ACTGCTCAGAAATTAGACTATAAGCTA	
DB	1324	ACTGCTCAGAAATTAGACTATAAGCTA	
QY	481	ACTAA\$GACCTCTAAATATGAAACTG	
DB	1384	ACTATGGACCTCTAAATATGAAACTG	
QY	541	AGTTTTG\$TTGATTTTTCCCTGAAAC	
DB	1444	AGTTTTG\$TTGATTTTCCCTGAAAC	
QY	601	TATAAGATAATGAAACCCTGACTCTA	
DB	1504	TATAAGATAATGAAACCCTGACTCTA	
QY	661	AAG 663	
DB	1564	AAG 1566	
RESULT 5			
DB	ABA76857	standard; DNA:	1817 BP.
XX	ABA76857;		
AC	ABA76857;		
XX	28-JAN-2002	(first entry)	
DE	Streptococcus pyogenes	polymerase	
XX	Detection; bacterial species; animal;		
FW	antibiotic resistance; ds.		
XX	Streptococcus pyogenes.		
OS	NZ501596-A.		
PN	NZ501596-A.		

XXX 29-JUN-2001. QY 361 GTATCAATCGATGGTACGCCAAGCTTATGATATTGAAACAAATAAAAAATGGTA 420
 XXX 12-SEP-1995; 95NZ-00501596. Db 1264 GTATCAATCGATGGTACGCCAAGCTTATGATATTGAAACAAATAAAAAATGGTA 1322
 XXX 12-SEP-1995; 95NZ-00501596. QY 421 ACTGGTCAGAAATGGACTATAAGTTAGAAATTCAGATTAAGCCAACTATAT 480
 (IDII-) IDI INFECTIO DIAGNOSTIC INC. Db 1324 ACTGGTCAGAAATGGACTATAAGTTAGAAATTCAGATTAAGCCAACTATAT 138
 Bergeron MG, Ouellette M, Roy PH; QY 481 ACTATGGACCTCTAAATGAACCTAACCTAGAATAAGAGAA 540
 WPI; 2001-615034/71. Db 1384 ACTATGGACCTCTAAATGAACCTAACCTAGAATAAGAGAA 144
 XXX Method for detecting target bacterial species in a sample, comprises
 detecting the presence or amount of bacterial nucleic acid amplified by a
 primer derived from bacterial DNA, specific for the target bacterial
 species. Claim 6; Page 107-108; 168pp; English.
 The invention relates to detecting target bacterial species suspected to
 be present in a sample, comprising contacting nucleic acids of target
 bacterial species with an amplification primer pair derived from a
 bacterial DNA fragment (ABA76825-ABA76861) specific for the target
 bacterial species but ubiquitous for different strains, amplifying the
 nucleic acid and detecting the presence or amount of an amplified
 sequence as an indication of the presence or amount of the target
 bacterial species. The invention includes primers and probes (ABA76662-
 ABA76984) against the target bacterial species, especially E.coli,
 K.pneumoniae, P.aeruginosa, P.mirabilis, S.aureus,
 S.pneumoniae, S.prophylticus, S.influenzae,
 M.catarrhalis and/or group A Streptococci producing exotoxin A gene spe
 A, suspected to be present in a sample which is obtained from human
 patients, animals, environment or food, and which consists of one or more
 bacterial colonies. Oligonucleotide probes and primers complementary to
 the bacterial genes encoding resistance to antibiotics such as bla(tem),
 bla(rib), bla(shv), aacB, aacC1, aacC2, aacC3, aacA4, meca, vanA, vanH,
 vanX, satA, aacA-aphD vat, vga, msra, sul and/or int (ABA76985-ABA77001)
 are also useful to identify commonly encountered and clinically important
 resistance genes. The invention provides a rapid method of bacterial
 identification that can be achieved, which reduces the time currently
 required for the identification of pathogens in the clinical laboratory
 Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 U; 0 Other;
 ISQ Query Match 99.8%; Score 661.4; DB 4; Length 1837;
 Best Local Similarity 99.8%; Pred. No. 2.1e-120;
 Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DDB 904 CAACAGAGCCCCGATCCAAGCCAACCTCACAGATCTAGTTAGTAAACCTTCAAAT 60
 XXX 1 CAACAGAGCCCCGATCCAAGCCAACCTCACAGATCTAGTTAGTAAACCTTCAAAT 60
 964 CAACAGAGCCCCGATCCAAGCCAACCTCACAGATCTAGTTAGTAAACCTTCAAAT 963
 XXX 61 ATATATTCTCTTATGAGGTGACCTGTACTACAGAAATGAACTGTGTGATCA 120
 964 ATATATTCTCTTATGAGGTGACCTGTACTACAGAAATGAACTGTGTGATCA 1023
 XXX 121 CTTTATCTCACCCTTAATATAATGTTCAGGGCCAAATTGTAAATTAAAACCT 180
 1024 CTTTATCTCACCCTTAATATAATGTTCAGGGCCAAATTGTAAATTAAAACCT 1083
 DB 181 GAACTTAAGAACCAAGAGATGGCAACTTATTAGATAAAACCGTTATTTATGGT 240
 XXX 1084 GAACTTAAGAACCAAGAGATGGCAACTTATTAGATAAAACCGTTATTTATGGT 1143
 DDB 241 GTAGATAATCACCCTCTGTTATTATGAAATGCGAAAGAGTCATGTATCAC 300
 XXX 1144 GTAGATAATCACCCTCTGTTATTATGAAATGCGAAAGAGTCATGTATCAC 1203
 CC 301 GGAGGGTAAATCATGAGGGATCATTTAGAAATCCTAAAGAGTAGTGTTAA 360
 CC 1204 GGAGGGTAAATCATGAGGGATCATTTAGAAATGCGAAAGAGTCATGTATCAC 1263
 XXX The present sequence is the DNA encoding Streptococcal pyrogenic exotoxin
 CC A (SPE-A), a bacterial superantigen toxin (SAG), used for the formulation
 CC of SPE-A vaccine SPEA42. The coding region of this SAG toxin is altered
 CC by site directed mutagenesis, introducing L42R mutation, that results in
 CC disruption of binding of the toxin to both the MHC class II or T-cell
 CC antigen receptor. SAG has anti-bacterial and autoimmunity inhibitory
 CC properties. Example 12; Page 92-94; 118pp; English.

CC sequence is useful for the production of SPE-A vaccines and specific
 CC antibiotics. This vaccine overcomes the disadvantages of the chemically
 CC inactivated toxoids and is designed to protect individuals against one or
 CC several related staphylococcal and streptococcal toxins. It is used for
 CC the diagnosis and treatment or amelioration of superantigen-associated
 CC bacterial infections

XX Sequence 1837 BP; 632 A; 249 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 3; Length 1837;
 Best Local Similarity 99.5%; Pred. No. 8; 8e-120;
 Matches 660; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 CAACAAAGACCCCGATCCAGCCAACTCAGAGTCAGTTAACCTTCAAAAT 60
 Db 904 CAACAAAGACCCGATCCAGCCAACTCAGAGTCAGTTAACCTTCAAAAT 963

Qy 61 ATATATTTCTTGTAGGGTGACCCGTGTACTCACAGATCTAGTTAACCTTCAAAAT 120

Db 964 ATATATTTCTTGTAGGGTGACCCGTGTACTCACAGATCTAGTTAACCTTCAAAAT 1023

Qy 181 GAACTTAAAGAAACGAGATGGCAACTTTAATTAAGGATAAAACGTTGATTTATGGT 240

Db 1084 GAACTTAAAGAAACGAGATGGCAACTTTAATTAAGGATAAAACGTTGATTTATGGT 1143

Qy 241 GTAGAAATTACCATCTCTGTATTATGTGAAAATCGAAAAGGAGTCAGTGTATCTAC 300

Db 1144 GTAGAAATTACCATCTCTGTATTATGTGAAAATCGAAAAGGAGTCAGTGTATCTAC 1203

Qy 301 GGAGGGTAAACAAATCAGAAAGGAATCATTTAGAAATTCTAAAGGATAAGTCGTAAA 360

Db 1204 GGAGGGTAAACAAATCAGAAAGGAATCATTTAGAAATTCTAAAGGATAAGTCGTAAA 1263

Qy 361 GATCATATCGATGGTATCAGGCTTAAACGCTTACATGTTGATTTGAAATAAAAATGTA 420

Db 1264 GATCATATCGATGGTATCAGGCTTAAACGCTTACATGTTGAAATAAAAATGTA 1323

Qy 421 ACTGCTCAAGAATTAGACTATAAGTAGAAAATATCTTACAGATAAAAGCAACTTAT 480

Db 1324 ACTGCTCAAGAATTAGACTATAAGTAGAAAATATCTTACAGATAAAAGCAACTTAT 1383

Qy 481 ACTAATGGACCTCTTAATATGAAACGGATAATAAGTTTACATCTAAAGGATAAAAGAA 540

Db 1384 ACTAATGGACCTCTTAATATGAAACGGATAAAAGTCTACATCTAAAGGATAAAAGAA 1443

Qy 541 AGTTTTGGTTGATTTCCTGAAACGAGATTCTCAATCTAAATTTTATGATA 600

Db 1444 AGTTTTGGTTGATTTCCTGAAACGAGATTCTCAATCTAAATCTTATGATA 1503

Qy 601 TATAAAGGATAATGAAACCGCTTACCTAACAGAGCCAATTCGTTACCTAACACC 660

Db 1504 TATAAAGGATAATGAAACCGCTTACCTAACAGAGCCAATTCGTTACCTAACACC 1563

Qy 661 AAG 663

Db 1564 AAG 1566

Qy RESULT 7

ID AEN84229 standard; cDNA; 1837 BP.

XX AC AEN84229;

XX DT 23-SEP-2002 (first entry)

XX DE Streptococcal pyrogenic exotoxin A vaccine SPEa42 coding sequence.

XX KW Exotoxin A; SPEa; SPEa42; superantigen; antigen; toxin; vaccine;

KW attenuation; mutant; gene; ss.
 XX Streptococcus pyogenes.
 OS Synthetic.

XX Location/Qualifiers

814..11569

/*tag= a /product= "SPEa42"

XX US6399332-B1.

XX PD 04-JUN-2002.

XX PF 01-SEP-1998; 98US-00144776.

XX PR 25-JUN-1997; 97US-00882431.

XX PA (USSA) US SEC OF ARMY.

XX PI Erlich RG, Olson MA, Bavari S;

XX WP1; 2002-546281/58.

DR P-PSDB; 12B79508.

XX Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases.

XX Disclosure; Col 61-63; 46PP; English.

XX The present sequence is the coding sequence of Streptococcus pyogenes vaccine SPEa42. The vaccine differs from the native SPE sequence by substitution of the Leu-42 residue by Arg. This mutation is expected to disrupt contact between the toxin and the HLA-DR receptor, reducing DR1 binding. SPEa42 can be expressed as a recombinant protein in Escherichia coli as a secreted protein or as a cytoplasmic product. No indicators of toxicity have been detected for the purified recombinant protein, and vaccine studies demonstrate that SPEa42 is highly antigenic, inducing protective immunity in a mouse animal model. The attenuated superantigen can be used to protect against superantigen toxin infections. Methods of producing and using altered superantigen toxins as vaccines, and in diagnosis and therapy are provided by the invention. A multivalent vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1, TSST-1 and SPE is predicted to provide protective immunity against the majority of bacterial superantigen toxins

XX SQ Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 6; Length 1837;
 Best Local Similarity 99.5%; Pred. No. 8.8e-120;
 Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CACAAAGACCCGATCCAGCAACTTACAGTGTAGTTAACCTTCAAAAT 60
 Db 904 CACAAAGACCCGATCCAGCAACTTACAGTGTAGTTAACCTTCAAAAT 963

Qy 61 ATATATTCCTTATGAGGGTCAACCTGTTACCTACAGAAATGTAATCTGTATCAA 120
 Db 964 ATATATTCCTTATGAGGGTCAACCTGTTACCTACAGAAATGTAATCTGTATCAA 1023

Qy 121 CTTTATATCTCACCATTAAATATATGTTAACCTTCAAAATATGATAAAATAAACCT 180
 Db 1024 CTATGATCTCACCATTAAATATGTTAACCTTCAAAATATGATAAAATAAACCT 1083

Qy 181 GACCTTAAAGACCAAGGATGCACCTTAATTAAGATAAAGACGTGATTTATGGT 240
 Db 1084 GACCTTAAAGACCAAGGATGCACCTTAATTAAGATAAAGACGTGATTTATGGT 1143

Qy 241 GTAGAATTAACATCTGTATTTATGAAATTCGAGAAAGTGCATGTACTAC 300
 Db 1144 GTAGAATTAACATCTGTATTTATGAAATTCGAGAAAGTGCATGTACTAC 1203

301 GGAGGGTAAACATGAGGGAAATCATTAGAAATTCCTAAAGATAAGTAGTCCTAA 360
 Db 1204 GGAGGGTAAACATGAGGGAAATCATTAGAAATTCCTAAAGATAAGTAGTCCTAA 1263
 Qy 361 GTATCAATCGATGGTANCMAAGCCTATCATTGATATTGAAACAAATAAAAATGTTA 420
 Db 1264 GTATCAATCGATGGTATICAAAGCCTATCATTGATATTGAAACAAATAAAAATGTTA 1323
 Qy 421 ACTGCCTCAAGAATTAGACTATAAACCTGAAATAATCTACAGATAATAAGCAACTAT 480
 Db 1324 ACTGCCTCAAGAATTAGACTATAAACCTGAAATAATCTACAGATAATAAGCAACTAT 1383
 Qy 481 ACTAATGGACCTTCTAAATGAAACTGGATAATAAGTCATACCTAGAAATAAGAA 540
 Db 1384 ACTAATGGACCTTCTAAATGAAACTGGATAATAAGTCATACCTAGAAATAAGAA 1443
 Qy 541 AGTTTTTGTTGATTTCCTGAACTGAATTACTCAATAATTCTATGATA 600
 Db 1444 AGTTTTTGTTGATTTCCTGAACTGAATTACTCAATAATTCTATGATA 1503
 Qy 601 TATAAGATAATGAAACGCTTGACTCAAACAAAGCCAAATTGAAAGTCACCTAACCC 660
 Db 1504 TATAAGATAATGAAACGCTTGACTCAAACAAAGCCAAATTGAAAGTCACCTAACCC 1563
 Qy 661 AAG 663
 Db 1564 AAG 1566

RESULT 8
 ACA61184 standard; DNA; 1837 BP.
 XX
 AC ACA61184;
 XX DT 11-AUG-2003 (first entry)
 DE DNA encoding streptococcal pyrogenic exotoxin A.
 XX Pyrogenic exotoxin A; ds; superantigen-associated bacterial infection;
 XX superantigen toxin; gene; vaccine.
 OS Streptococcus sp.
 Key Location/Qualifiers
 FT 814 .1569
 FT /*tag= a
 FT /product= "Pyrogenic exotoxin A"
 XX US2003009015-A1.
 PD 09-JAN-2003.
 XX 25-JUN-1997; 97US-00882431.
 XX 25-JUN-1997; 97US-00882431.
 XX (ULRICH R. G.
 PA (OLSON M. A.
 PA (BAVARI S.
 PI Ulrich RG, Olson MA, Bavarri S;
 XX WPI: 2003-401542/38.
 DR P-PSDB; ABU10088.

XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC Class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX Claim 9; Page 32-34; 50pp; English.
 PS XX

CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigen to MHC class II or T-cell antigen receptors. The present
 CC sequence represents DNA encoding streptococcal pyrogenic exotoxin A
 XX
 SQ Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;
 Query Match 99.3%; Score 658.2; DB 7; Length 1837;
 Best Local Similarity 99.5%; Pred. No. 8.8e-120;
 Matches 660; Conservative 0; Mis matches 3; Indels 0; Gaps 0;
 CC
 Qy 1 CAACAGACCCGATTCAGAGATAGTTAGTTAAACCTTCAAAT 60
 Db 904 CAACAGACCCGATTCAGAGATAGTTAGTTAAACCTTCAAAT 963
 Qy 61 ATATATTTCTTTATGAGGTGACCCGTACTCACGAGATGTCAAATCTGTGATCAA 120
 Db 964 ATATATTTCTTTATGAGGTGACCCGTACTCACGAGATGTCAAATCTGTGATCAA 1023
 Qy 121 CTTTTATCTACCCATTAAATATAATATGTTTCAGGCCAAATTAGTAAATTAAACT 180
 Db 1024 CTTAGATCTCACGATTAAATATGTTTCAGGCCAAATTAGTAAATTAAACT 1083
 Qy 181 GAACTTAAGACCAAGAGATGGCACTTTTAAAGATAAAAGCTGATATTATGGT 240
 Db 1084 GRACTTAACTCATCTCTGTTATTATGTTAAATGCAAAAGGAGTGTGATATTATGGT 1143
 Qy 241 GTAGATAATTACCATCTCTGTTATTATGTTAAATGCAAAAGGAGTGTGATCTAC 300
 Db 1144 GTAGATAATTACCATCTCTGTTATTATGTTAAATGCAAAAGGAGTGTGATCTAC 1203
 Qy 301 GGAGGGTACAAACATGAGGAAATCATGAGGAACTTAAAGCTAAAGAGTACTTAA 360
 Db 1204 GGAGGGTACAAACATGAGGAACTTAAAGATGCTCTAAAGATGCTCTTAA 1263
 Qy 361 GTATAATCGATGGTATCCAAGCCTATCATTGATATGAAACAATAAAATGGTA 420
 Db 1264 GTATAATCGATGGTATCCAAGCCTATCATTGATATGAAACAATAAAATGGTA 1323
 Qy 421 ACTGCCTCAAGAATTGACTATAAGCTTAAAGATAATGCAAACTTAT 480
 Db 1324 ACTGCCTCAAGAATTGACTATAAGCTTAAAGATAATGCAAACTTAT 1383
 Qy 481 ACTATGGACCTCTAAATATGAAACTGGATATATGTTCATACCTAAAGANTAAAGA 540
 Db 1384 ACTATGGACCTCTAAATGTTAAATGAAACCTCATCCATAGAAATAAGA 1443
 Qy 541 AGTTTTGGTTGATTTTCCCTGAAAGGAAATTACTCAATAATCTATGATA 600
 Db 1444 AGTTTTGGTTGATTTTCCCTGAAAGGAAATTACTCAATAATCTATGATA 1503
 Qy 601 TATAAGATAATGAAACGCTTGACTCAAACACAGCCAAATTGAGGTCTACCTAACACC 660
 Db 1504 TATAAGATAATGAAACGCTTGACTCAAACAGCCAAATTGAGGTCTACCTAACACC 1563
 Qy 661 AAG 663
 DR 1564 AAG 1566

RESULT 9
 AAD56771 standard; DNA; 1837 BP.
 ID AAD56771
 XX AC
 AC AAD56771;
 XX

DT 06-OCT-2003 (first entry)

XX Streptococcus pyogenes pyrogenic exotoxin A (SpeA) DNA.

XX Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA.

KW gene therapy; gene; ds.

XX

OS Streptococcus pyogenes.

XX

Key Location/Qualifiers

CD5 814..1569 /*tag= "Streptococcus pyogenes SpeA protein"

FT /product= "Streptococcus pyogenes SpeA Protein"

FT /transl_except= (pos 1901..903, aa Met)

FT /note= "This exception occurs only when decoding SEQ ID NO: 26 (RAE37687)"

FT peptide 814..900 /*tag= b

FT peptide 901..1566 /*tag= c

FT peptide 1567..1587 /*product= "Streptococcus pyogenes mature SpeA protein"

XX WO2003056015-A1.

PN XX

PD 10-JUL-2003.

XX 26-NOV-2001; 2001WO-US046540.

XX 26-NOV-2001; 2001US-00002784.

PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX

PI Ulrich RG;

XX

PS WPI; 2003-492125/46.

DR P-PSDB; AAE37683, AAE37687

XX

CC New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.

XX

PS Claim 4; Page 128-129; 141pp; English.

XX

CC The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin A (SpeA) DNA. This sequence is used in the invention.

SQ Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.3%; Score 658.2; DB 8; Length 1837;

Best Local Similarity 99.5%; Prod. No. 8.8e-120;

Matches 660; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC

YQ 1 CAACAGAGCCCCATCAAGCCAACTTCAGATCTAGTTAGTAAACCTTCATAAT 60

Db 904 CAAAGAACCCCATCAAGCCAACTTCAGATCTAGTTAGTAAACCTTCATAAT 963

YQ 61 ATATATTTCCTTATGAGGGTGAACCTGTACTCAGAGAATCTGTTGATCAA 120

Db 964 ATATATTTCCTTATGAGGGTGAACCTGTACTCAGAGAATCTGTTGATCAA 1023

YQ 181 GAATTTAGAACCAAGAGAGACTTATTAAGGTAAACGTGATATTATGGT 240

Db 1084 GAACTTAAAGAACCAAGAGAGACTTATTAAGGTAAACGTGATATTATGGT 1143

YQ 241 GTAGAAATTACCATCTCTTATTATGAAAAATGCAGAACGAGTCATGATCTAC 300

Db 1144 GTAGAAATTACCATCTCTGTTATTGTGAAATGCGAAATGGACTGCGATCTAC 1203

QY 301 GGAGGGTAAATCATGAGGAATCATTAAGATCTAAAGATCTCGTTAAA 360

Db 1204 GGAGGGTAAATCATGAGGAATCATTAAGATCTCGTTAAA 1263

QY 361 GTATCAATCGTGTATCCAAAGCCATCATTGATATTGAAATAAATGGTAA 420

Db 1264 GTATCAATCGTGTATCCAAAGCCATCATTGATATTGAAATAAATGGTAA 1323

QY 421 ACTGCTCAAGAATTAAGCTTACAGATAATAGCAACTATAT 480

Db 1324 ACTGCTCAAGAATTAAGCTTACAGATAATAGCAACTATAT 1383

QY 481 ACTTAATGACCTCTTAATATGAACTGGATATAAGTICATACCTAAGATAAGAA 540

Db 1384 ACTTAATGACCTCTTAATATGAACTGGATATAAGTICATACCTAAGATAAGAA 1443

QY 541 ACTTTTGGTTGATTTTCCTGAACTGATTTACTCATTAATATCTTATGATA 600

Db 1444 ACTTTTGGTTGATTTTCCTGAACTGATTTACTCATTAATATCTTATGATA 1503

QY 601 TATAAAGATAATGAAAGCCTTCATCTAACACAGCCAAATTGAACTCTAACACC 660

Db 1504 TATAAAGATAATGAAAGCCTTCATCTAACACAGCCAAATTGAACTCTAACACC 1563

RESULT 10

ACD28901

ID ACD28901 standard; DNA; 1837 BP.

XX

AC ACD28901;

XX DT 27-AUG-2003 (first entry)

XX Streptococcus pyrogenic toxin a L42R mutant, DNA.

DE XX

KW SPEA; streptococcus pyrogenic enterotoxin a; gene; mutant; vaccine; ds;

KW superantigen toxin; MHC; superantigen-associated bacterial infection;

KW bacterial infection; antibody.

XX

OS Streptococcus sp.

OS Synthetic.

XX

FH Key

CDS Location/Qualifiers

814..1569 /*tag= a

FT /product= "SPEA L42R"

FT sig_peptide 814..903

FT /*tag= b

FT mat_peptide 904..1566

FT /*tag= c

FT /label= Mature SPEA L42R

XX US20030316644-A1.

PN US20030316644-A1.

XX US20030316644-A1.

PD 20-FEB-2003.

XX

PF 26-NOV-2001; 2001US-00002784.

XX

PR 25-JUN-1997; 97US-00882431.

PR 01-SEP-1998; 98US-00144776.

XX

PA (ULRI-) ULRICH R G.

XX PI Ulrich RG,

XX DR WPI; 2003-492125/46.

DR P-PSDB; ABU62331.
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX

Claim 4; Page 36-37; 66pp; English.

XX The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection), treating/ameliorating a superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and SPEb). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence encodes the L42R (with reference to the mature protein) mutant of SPEa.

XX Sequence 1837 BP; 638 A; 318 C; 248 G; 638 T; 0 U; 0 Other;

Query Match 99.0%; Score 656.6; DB 8; Length 1837;
 Best Local Similarity 99.4%; Pred. No. 1.8e-119;
 Matches 659; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAAAGAACCGATTCAGGCCAATTCTAGTTAGTTAGTAAACCTTCATAAT 60
 Db 904 CAAAGGCCCCGATCCAGGCCACTTCAGATCTAGTTAGTAAACCTTCATAAT 963

QY 61 ATATATTCTTTATGAGGGTACGTGAAATCTGTGATCAA 120
 Db 964 ATATATTCTTTATGAGGGTACGTGAAATCTGTGATCAA 1023

QY 121 CTTTATCACCATTAAATAATATAATGTTTCAGGGCCAATTCTAGATAAATAAACT 180
 Db 1024 CTTAGATCTACGATTAAATAATGTTTCAGGGCCAATTCTAGATAAATAAACT 1083

QY 181 GAACTTAAGGAACTCATGAAGGGAAATCTAGTTAGATAAAACGTGTTATGTT 240
 Db 1084 GAACTTAAGGAACTCATGAAGGGAAATCTAGTTAGATAAAACGTGTTATGTT 1143

QY 241 GTAGAATTAACCATCTCGTATTATGAAATGCGAAAGGAGTCATGTTAC 300
 Db 1144 GTAGAATTAACCATCTCGTATTATGAAATGCGAAAGGAGTCATGTTAC 1203

QY 301 GGAGGGGTACAATCATGAAGGGAAATCTAGTTAGATAAAACGTGTTAA 360
 Db 1204 GGAGGGGTACAATCATGAAGGGAAATCTAGTTAGATAAAACGTGTTAA 1263

QY 361 GTATCAATCGTGTATCAAGCTATATTGATATTGAAATGCGAAATGTTAA 420
 Db 1264 GTATCAATCGTGTATCAAGCTATATTGATATTGAAATGCGAAATGTTAA 1323

QY 421 ACTGTCAGAAATTAGACTAACTGAACTTACGATAATAGCAACTAT 480
 Db 1324 ACTGTCAGAAATTAGACTAACTGAACTTACGATAATAGCAACTAT 1383

QY 481 ACTATGGACCTCTAAATGAAACTGGATATAAAGCTCATCCDAGATAAAGCA 540
 Db 1384 ACTATGGACCTCTAAATGAAACTGGATATAAAGCTCATCCDAGATAAAGCA 1443

QY 541 AGTTTTGGTTGATTTCCTGAACTGAAATTACTCAATTAATCTGTATA 600
 Db 1444 AGTTTTGGTTGATTTCCTGAACTGAAATTACTCAATTAATCTGTATA 1503

QY 601 TATAAGATAATGAAACGCTTGAACACAGCCAAATTGAAAGTCTACCTAACAAAC 660
 Db 1504 TATAAGATAATGAAACGCTTGAACACAGCCAAATTGAAAGTCTACCTAACAAAC 1563

Db 661 AAG 663
 Db 1564 AAG 1566

RESULT 11.
 ACID:8908
 ID: ACID:8908 standard; DNA; 1419 BP.

DEPOT: SPEA L42R/SPEB C47S mutant fusion protein, DNA.

KW SPEB; streptococcus pyrogenic enterotoxin; gene; mutant; vaccine; ds; superantigen toxin; Mhc; superantigen-associated bacterial infection; bacterial infection; antibacterial; SPEB.

OS Streptococcus sp.

OS Synthetic.

XX Key
 PH CDS
 FT 1. .tag=^
 FT /product= "SPEA L42R/SPEB C47S"
 FT /transl_except= (pos:298 .306 aa:Ile-Gly)
 FT /transl_except= (pos:634 .642 aa:Thr-Gln)
 FT /transl_except= (pos:1162 .1170 aa:Ser-Gln)
 FT /transl_except= (pos:1228 .1236 aa:Gly-Gly)

XX Location/Qualifiers
 1. .tag=^
 FT /product= "SPEA L42R/SPEB C47S"
 FT /transl_except= (pos:298 .306 aa:Ile-Gly)
 FT /transl_except= (pos:634 .642 aa:Thr-Gln)
 FT /transl_except= (pos:1162 .1170 aa:Ser-Gln)
 FT /transl_except= (pos:1228 .1236 aa:Gly-Gly)

XX US2003036644-A1.

XX DD 20-FEB-2003.
 XX RF 26-NOV-2001; 2001US-00002784.
 XX PR 25-JUN-1997; 97US-00882431.
 PR 01-SEP-1998; 98US-00144776.
 XX PA (ULRICH) ULRICH R. G.
 XX PI Ulrich RG;
 XX DR WPI; 2003-492125/46.
 DR P-PSDB; ABU62335.

XX New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.

XX Claim 6; Page 39-40; 68pp; English.

CC The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising a vector and an isolated and purified altered superantigen toxin associated bacterial infection for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection), treating/ameliorating a superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and SPEb).

Qy 421 ACTGCTCAGAATTAGACTATAAGTAAAGATAATCTACAGATAATAAGGAACCTAT 480
 Db 424 ACTGCTCAGAATTAGACTATAAGTAAAGATAATCTACAGATAATAAGGAACCTAT 483
 Qy 481 ACTAATGGACCTCTAAATATGAACTCTGATATAAGTTGATACCTAAAGATAAGAA 540
 Db 484 ACTAATGGACCTCTAAATATGAACTCTGATATAAGTTGATACCTAAAGATAAGAA 543
 Qy 541 AGTTTGTGTTGATTTCCTGAAACAGCAATTACTCATCTAAATCTTGATA 600
 Db 544 AGTTTGTGTTGATTTCCTGAAACAGCAATTACTCATCTAAATCTTGATA 603
 Qy 601 TATAAAGTAATGAAAGCGTTSAGCTAAACACAAGCCAAATTGAAAGTCTACTAAACC 660
 Db 604 TATAAAGTAATGAAAGCGTTSAGCTAAACACAAGCCAAATTGAAAGTCTACTAAACC 663
 Qy 661 AAG 663
 Db 664 AAG 666

RESULT 13
 ACNA64700 standard; DNA; 1031 BP.
 XX DT 18-JUN-2003 (First entry)
 DE S. Pyogenes exotoxin (SPB4) gene.
 XX KW Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer;
 XX KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;
 XX KW Yumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 OS XX Streptococcus pyogenes.
 XX PS US2002177551-A1.
 HD 28-NOV-2002.
 XX HF 30-MAY-2001; 2001US-00870759.
 PR 31-MAY-2000; 2000US-0208128P.
 PA (TERM/) TERMAN D S.
 XX PI Terman DS;
 XX DR WPI-2003-361759/34.
 PS P-PSDB-A-BU79074.

A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces energy or apoptosis in T cells and antigen presenting cells.

Disclosure: Page: 167pp; English.

The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces energy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) tumourcidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphoinositols, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (SAg) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which

inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumourcidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumourcidal immunocyte population, and administering the tumourcidally activated immunocytes to the host), producing (M3) a tumourcidal APC population ex vivo in a mammal (by allowing a tumour associated lipid to contact APCs, in which receptors for the tumour associated lipids are inactivated or deleted to produce a tumourcidally activated population, and administering APs to the host), producing a tumourcidal T cell population ex vivo in a mammal (by allowing a tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumour associated antigens, are deleted or functionally deactivated to produce a tumourcidal population of T cells, and administering the tumourcidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumourcidally activated T cells to the host), treating tumour associated antigens by tumour associated antigens (M4) a cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumourcidal T cell population in vivo in a mammal (by allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence encodes a bacterial superantigen Protein (e.g., a staphylococcal enterotoxin). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US Patent Office website at "seqdata.uspto.gov/sequence.html?docID=20020177551"
 XX SQ Sequence 1031 BP; 381 A; 146 C; 162 G; 342 T; 0 U; 0 Other;
 Query Match 87.9%; Score 582.6; DB 7; Length 1031;
 Best Local Similarity 97.1%; Pred. No. 5.3e-105;
 Matches 636; Conservative 0; Mismatches 14; Indels 5; Gaps 4;
 Qy 10 CCCGATCCAGCCACCTTCAAGACAGTAGTTAGTTAAACCTCAAATATAATT 69
 Db 178 CCCGGCCAGCCGATTTAAAGACTTATTTATTT -ANACCTCTNATAATTT 236
 Qy 70 CTTTATGAGGTGACCCCT-GTTACTCACGAAATCTGTGTGAACTTTATC 128
 Db 237 CTTTATGAGGTGACCCGTACTCACGAAATCTGTGAACTTTATC 296
 Qy 129 TCACCCATTAAATATAATATGTTTCAGGGCCAATTATGATAAATTAACACTAA 188
 Db 297 ACACATTAAATATAATGTTCAGGCCAAATATGATAAAUTAAAATGAACTTAA 356
 Qy 189 GAACCAAGCATGGCAACTTATTAAGATAAAACGTGATAATTATGGTGAATA 248
 Db 357 GAACCAAGCATGGCAACTTATTAAGATAAAACGTGATAATTATGGTGAATA 416
 Qy 249 TTACCATCTCTGTATTTATGTGAAATTCGAAAGGACTGCATGATCTACGGGGGT 308
 Db 417 TTACATCTCTGTATTTATGTGAAATTCGAAAGGACTGCATCTACGGGGGT 476
 Qy 309 AACATCATGAGGGAATCATTTAGAAATTCTAANANGATCTGTTAAACTTCAT 368
 Db 477 AACATCATGAGGGAATCATTTAGAAATTCTAANAGATCTGTTAAACTTCAT 536
 Qy 369 CGATGTGATCTCCAGCCATCATTTGATATTGAAACAAATAAAATGGTAACTGCTCA 428
 Db 537 CGATGTGATCCAAAGCCATCATTTGATATTGAAACAAATAAAATGGTAACTGCTCA 594
 Qy 429 AGATAGTAAAGTAAAGTGTGAAATCTACAGATAATAACCAACTATACTAATGG 488
 Db 595 AGATAG-CTATACAGTTGAAATATCTACAGATAATAACCAACTATACTAATGG 653

CC 489 ACCCTCTTAATATGAAACTGGATATAAAGTTACCTAAGAATAAGAAAAGTTTG 548
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC 654 ACCCTCTTAATATGAACTGGATATAAAGTTACCTAAGAATAAGAGTTTG 713
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC 519 GTTGTGTTTTCCTGACCGAAATTACTCATCATAATCTTATGATATAAGA 608
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC 714 GTTGTGTTTTCCTGACCGAAATTACTCATCATAATCTTATGATATAAGA 773
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC 699 TAATGAACGCTTGACTCAAACACAAGGCCAAATTGAAGTCTACACCAAG 663
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC 774 TAATGAACGCTTGACTCAAACACAAGGCCAAATTGAAGTCTACACCAAG 828
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
 ACA64696 standard; DNA; 1095 BP.
 XX
 AC ACA64696;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE S. aureus SEC (staphylococcus enterotoxin C) gene.
 XX
 KW Superantigen; ds; gene; SAG; staphylococcal enterotoxin; tumour; cancer;
 KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; energy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.
 XX
 OS Staphylococcus aureus.
 XX
 PN US2002177551-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 30-MAY-2001; 2001US-00870759.
 XX
 PR 31-MAY-2000; 2000US-0208128P.
 PR
 PA (TERBM/) TERMAN D S.
 XX
 PI Terman DS;
 XX
 WPI: WPI-3-361759/34.
 DR P-NSDB; ABU70070.
 XX
 PT A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces energy or apoptosis
 PT in T cells and antigen presenting cells.
 XX

PS Disclosure: Page: 167PP; English.
 XX
 CC The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phospholipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteolipopolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidally

activated immunocytes to the host), producing (M3) a tumouricidal APC population ex vivo in a mammal (by allowing a tumour associated lipid to contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering (Apes to the host), producing a tumour associated lipid to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population comprising allowing a
 CC superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC present invention provides methods and compositions useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC constructs with anti-tumour proteins or motifs. The present
 CC sequence encodes a bacterial superantigen protein (e.g. a staphylococcal
 CC enterotoxin). Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format from
 CC the US Patent office website at
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 SQ Sequence 1095 BP; 433 A; 125 C; 185 G; 352 T; 0 U; 0 Other;

Query Match	Score 25.2%	DB 7;	Length 1095
Best Local Similarity 59.0%	Prd. No. 1e-23;		
Matches 382; Conservative 0; Mismatches 226; Indels 39; Gaps 4;			
QY 56 AAATATATATTTCTCTTTATGAGCTGACCCCTTTACTCACGGAATTGAAATCTGTG 115			
Db 263 AAATATGAAAGTTTATATGATCATTTATGATCATTTATGAACTTAACTTGTGAG 322			
QY 116 ATGAACTTTTATCACCATTATAATTTCTTCAAGG-----GCCAAATTATG 166			
Db 323 ATTAATTTGGACATGTTATTTATGATCATTTATGATAAAACTGAAATTATG 382			
QY 167 ATAAATTTAAACTGAACCTTAAACCAAGAGATGGCAACTTTATAAGGATAAAACG 226			
Db 383 ACAAATGAAACAGAGTTTAAATGAGTTAGCAAGAGTACAAAGATGAATGTAG 442			
QY 227 TGTATTTATGGTAGATAATCCATTCTCTGTATTAT-----GCCAAATTATG 268			
Db 443 TGTATGTGTATGATCAAAATTCTATGFAAACTGCTATTTCATCCAAATGTAG 502			
QY 269 GTGAAATCAGAAGAGACTGATGCTGATTTACGGAGGGTAAAGATGAAATGGAAATC 328			
Db 503 GTAAAGTTACAGGTGCGAAACTGTGATGATGATGATGATGAACTAACACC 562			
QY 329 ATTPGAATTCCTA-----AAAAGATAGTCGTTAAACTATCATCGATGGTATCCAAA 382			
Db 563 ACTTGTATGGAACTACAAATGTACTTAAGGTAAATTAAGAATGAAATGAA 622			
QY 383 GCCTCATCTGATGATGAAACATAAAAAATGGTAACTGCCTCAAGAATTGACTATA 442			
Db 623 CAATTCCTTGTAACTGCAAACTGATAAGAAACTGTACAGCTCAAGACTAACATA 682			
QY 443 AAGTGTAGAAATAAAGTCATACCTAAAGATAAGAAGTTGGTTGATTTTCC 502			
Db 683 AGCTTAGGAAATTGTTAAATTAATGAAATGTTGATGTTGATGTTGATGTTGATCATG 742			
QY 503 AACCTGGATAATAAAGTCATACCTAAAGATAAGAAGTTGGTTGATGTTGATGTTGATGATG 562			
Db 743 AACAGGATATAAAATTATGAAATGAAACTTGTGATGATAAAAGATAATGAAA 802			
QY 563 CTGAAACCAG-----AATTTACTCAATCTAAATCTATGATAATAAGATAATGAAA 616			

Db 803 CTGACCAAGGGATAAAGTTGACCAATCTAAATATTAAATGATGTACAACGACATAAAA 862
 QY 617 CGCTTGACTCAAAGCACAAATGCAAGCCAAAGCTTACCTAACCCAG 663
 Db 863 CGGTGATCTAAAAGTGTGAAGATAAGTCACCTTACAAAG 909

RESULT 15
 AAT45698 standard; cDNA; 773 BP.
 XX AC AAT45698;
 DT 08-MAR-1997 (first entry)
 XX DE Staphylococcus enterotoxin B cDNA.
 XX KW Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell; lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine; adjuvant; ss.
 XX OS Staphylococcus sp.
 XX Key Location/Qualifiers
 FT 1. .768
 FT /tag= a
 FT /note= "the full-length coding sequence can be used in nucleic acid-based therapeutic compns. of the invention"
 FT sig_peptide 1. .45
 FT primer_bind /tag= b
 FT complement (37. .61)
 FT /tag= d
 FT mat_peptide 46. .765
 FT /tag= c
 FT /note= "the coding sequence for the mature protein can be used in nucleic acid-based therapeutic compns. of the invention"
 FT primer_bind 754. .768
 FT /tag= e
 FT /note= "SEB-S amplification primer binding site"
 XX WO9633656-A1.
 XX PD 21-NOV-1996.
 XX PF 20-MAY-1996; 96W0-US007432.
 XX PR 18-MAY-1995; 95US-00446918.
 XX PR 29-DEC-1995; 95US-00580806.
 XX PA (NIAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX Dow SW, Elmslie RB, Potter TA;
 PI DR; 1997-011857/01.
 DR p-NSDB; AA06737.

CC comprising an immunogen and a superantigen nucleic acid can be used with DNA-based vaccines
 CC Sequence 773 BP; 305 A; 94 C; 133 G; 241 T; 0 U; 0 Other;
 SQ Query Match 25.2%; Score 166.8; DB 2; Length 773;
 Best Local Similarity 59.1%; Pred. No. 1.3e-23;
 Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;
 QY 56 AAAATATATATTCTTCTTGTGAAATCTGTG 115
 Db 113 AAAATGAGTTGTATGATGAAATACGTTAAATCTATAG 172
 QY 116 ATCAACTTATCTCACCATTAAATATATATGTTCTCGGCCA-----ANTATTG 166
 Db 173 ATCAATTCTATACCTTGTACTTAATCTTAAAGACACTAAGTTGGGATTATG 232
 QY 167 ATAATTAATAAACCTAACCTAAAGAACAGATGCAACTTTTAAAGGATAAAACG 226
 Db 233 ATATGTTGGAGTCGAATTAAACAGATTGCTGATAATAACAGATATAACAGATATAACG 292
 QY 227 TTGATATTATGGTAGATAATTACCATCTCTGTATTATGTGAAAA----- 275
 Db 293 TAGATGTTGGAGCTAAATTATTTAAATGTTCTAAATGTTAAACGATGATA 352
 QY 276 -----TGCAGAAGGAGTCATGATCTACGGAGGGTAACAAATCATG 319
 Db 353 TTAATCGCATCAAMCTGAAACAAAACACTGTATGTTGAAACTGGCATA 412
 QY 320 AAGGAAATCTTGTAAAGTCTAAAGTCAATGATGTTAC 379
 Db 413 ATGGAAACCAATTAGATAATATAGAGPATTACTGTCGGPATTTGAGATGGTAAA 472
 QY 380 AAAGGCTATATTGATAATGAAACAAATAAAATGGTAACTGCTCAGAATTAGACT 439
 Db 473 ATTATTATCTTGTACGTACAACATAATAGAAAGGTGACTCTGTCAGAATTAGATT 532
 QY 440 ATAAGTTGAAAATATCTACAGATAATAGCAACTATACATAATGACCTCTAAAT 499
 Db 533 ACCAACTCTCAATTCTGAAATAAAACTCTGAAATTAAACACTCGCCPT 592
 QY 500 ATGAAACTGGATATAAGTCTACCTAAGATAAAAGTTGGTTGTTTTT 559
 Db 593 ATGAAACGGGATATTAATTATA---GAAAATGGAATAGCTTGGTGTACATGA 649
 QY 560 TCCCTGAAACCG----AATTAACTCAATCTAAATCTATGATATAAGATAATG 613
 Db 650 TGCCCGCACCAGGAGTAATTIGCAACCTAAATTAATGTCACATACATA 709
 QY 614 AAACCTTGACTCAAACAAAGCCAATGAACTCTACCTAACACCAAG 663
 Db 710 AAATGGTGGATTCAAAGATGTGAAATGAGTTCTACGAAAG 759

Search completed: September 3, 2004, 17:26:20
 Job time : 377 secs

XX Recombinant molecule encoding super antigen and opt. cytokine or chemokine - controls activity of effector cells (T cells, monocytes, natural killer cells), used for gene therapy of cancer.
 XX Example 1: Page 95-96; 13ipp; English.
 XX A cDNA clone (AAT45698) codes for staphylococcal enterotoxin B (AAW06737) superantigen. Nucleic acids encoding superantigens (see also AAT45699 and AAT45706) can be utilised in the gene therapy of cancer, infectious diseases and immunological disorders. The nucleic acid, optionally in combination with cytokine or chemokine nucleic acids, is delivered to an animal using e.g. liposomes. It acts by controlling the activity of effector cells, such as T-cells, macrophages, monocytes and/or natural killer cells. Localised prodn. of an effective but non-toxic amount of encoded proteins allows safe treatment of the animal. Adjuvants

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OM nucleic - nucleic search, using sw model

Run on: September 3, 2004, 18:16:37 ; Search time 422 Seconds

(without alignments)
7809.322 Million cell updates/sec

Title: US-10-625-221-12_COPY_918_1580

Perfect score: 663

Sequence: 1 caacaagaccggatccaag.....aatgtctacttaacaaccagg 663

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3267054 seqs, 2485319735 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published Applications NA:*

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19: /cgmn_6/_ptodata/2/_pubna/_us60_pubcomb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	663	100.0	1851	8 US-08-973-391A-12	Sequence 12, Appl
2	663	100.0	1851	13 US-09-308-830-12	Sequence 12, Appl
3	661.4	99.8	1837	9 US-09-452-509-33	Sequence 33, Appl
4	661.4	99.8	1837	15 US-10-121-120-33	Sequence 33, Appl
5	658.2	99.3	1837	8 US-08-882-131-15	Sequence 15, Appl
6	655.6	99.0	1837	15 US-10-002-784A-15	Sequence 23, Appl
7	651.8	98.3	1419	15 US-09-705-784A-23	Sequence 19, Appl
8	582.6	87.9	1031	9 US-09-870-759-19	Sequence 19, Appl
9	582.6	87.9	1031	10 US-09-751-108A-19	Sequence 11, Appl
10	167.4	25.2	1095	9 US-09-870-759-11	Sequence 11, Appl
11	167.4	25.2	1095	10 US-09-751-708A-11	Sequence 11, Appl
12	166.8	25.2	773	13 US-10-354-948-1	Sequence 1, Appl
13	166.8	25.2	801	9 US-09-870-759-1	Sequence 1, Appl
14	166.8	25.2	801	10 US-09-751-708A-1	Sequence 1, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SEQ ID	Query	Match length	DB ID	Description
1	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	Organism: Streptococcus pyogenes
2	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	FEATURE: ;
3	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	NAME/KEY: CDS
4	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	LOCATION: (82B)::(1583)
5	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	OTHER INFORMATION: ;
6	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	US-08-973-391A-12
7	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	RESULT 1
8	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; Sequence 12, Application US-08-973-391A-12
9	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; Publication No. US2002-0054487A1
10	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; GENERAL INFORMATION: ;
11	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; APPLICANT: Schlievert, Patrick M.
12	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; ROGIANI, Manuela
13	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; STOHR, Jennifer
14	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; APPLICANT: Ohlendorf, Douglas
15	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
16	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; CURRENT APPLICATION NUMBER: US-08-973-391A
17	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; PCT REFERENCE: 600-311UWO
18	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; CURRENT FILING DATE: 1998-03-12
19	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; PRIOR FILING DATE: 1996-06-07
20	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; PRIOR APPLICATION NUMBER: US-08/480,261
21	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; NUMBER OF SEQ ID NOS: 13
22	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; SOFTWARE: PatentIn version 3.1
23	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; SEQ ID NO: 12
24	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; LENGTH: 1851
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26	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; ORGANISM: Streptococcus pyogenes
27	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; FEATURE: ;
28	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; NAME/KEY: CDS
29	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; LOCATION: (82B)::(1583)
30	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; OTHER INFORMATION: ;
31	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; US-08-973-391A-12
32	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	RESULT 1
33	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; Sequence 12, Application US-08-973-391A-12
34	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; Publication No. US2002-0054487A1
35	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; GENERAL INFORMATION: ;
36	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; APPLICANT: Schlievert, Patrick M.
37	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; ROGIANI, Manuela
38	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; STOHR, Jennifer
39	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
40	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; CURRENT APPLICATION NUMBER: US-08/973-391A
41	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; PCT REFERENCE: 600-311UWO
42	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; CURRENT FILING DATE: 1998-03-12
43	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; PRIOR FILING DATE: 1995-06-07
44	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; NUMBER OF SEQ ID NOS: 13
45	CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	60	1 CAACAGACCCGATCCAAGCCAACTTCAGAGTGTAAACCTTCAAAT	; SOFTWARE: PatentIn version 3.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	663	100.0	1851	8 US-08-973-391A-12	Sequence 12, Appl
2	663	100.0	1851	13 US-09-308-830-12	Sequence 12, Appl
3	661.4	99.8	1837	9 US-09-452-509-33	Sequence 33, Appl
4	661.4	99.8	1837	15 US-10-121-120-33	Sequence 33, Appl
5	658.2	99.3	1837	8 US-08-882-131-15	Sequence 15, Appl
6	655.6	99.0	1837	15 US-10-002-784A-15	Sequence 23, Appl
7	651.8	98.3	1419	15 US-10-002-784A-23	Sequence 19, Appl
8	582.6	87.9	1031	9 US-09-870-759-19	Sequence 19, Appl
9	582.6	87.9	1031	10 US-09-751-108A-19	Sequence 11, Appl
10	167.4	25.2	1095	9 US-09-870-759-11	Sequence 11, Appl
11	167.4	25.2	1095	10 US-09-751-708A-11	Sequence 11, Appl
12	166.8	25.2	773	13 US-10-354-948-1	Sequence 1, Appl
13	166.8	25.2	801	9 US-09-870-759-1	Sequence 1, Appl
14	166.8	25.2	801	10 US-09-751-708A-1	Sequence 1, Appl

RESULT 2
US-09-308-830-12
; Sequence 12, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION : MUTANTS OF STREPTOCOCCAL TOXIN A
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308, 830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997

QY 61 ATATATTTCCTTATGGGGTACCCGTACTCACCAGAAATGCGAAATCTGTGATCAA 120
D5 978 ATATATTTCCTTATGGGGTACCCGTACTCAGGAAATGCGAAATCTGTGATCAA 1037
QY 121 CTTTTATCTCACCATTATAATATGTTCAAGGCCAAATTATGATAAATTAAAAGCT 180
D5 1038 CTTTTATCTCACCATTATAATATGTTCAAGGCCAAATTATGATAAATTAAAAGCT 1097
QY 181 GRACTTAGAACGACGAGATGGCAGCTTATAAGATAAACCTGATATTATGGT 240
D5 1098 GAACTTAGAACAGATGGCAGCTTATAAGATAAACCTGATATTATGGT 1157
QY 241 GTAGAAATTACCATCTGTATTATGTGAAATGAGAAGGGTCACTATAC 300
D5 1158 GTAGAAATTACCATCTGTATTATGTGAAATGAGAAGGGTCACTATAC 1217
QY 301 GGAGGGTAACAAATCTGAAGGGAAATCTTAAAGATAATCGTAA 360
D5 1218 GGAGGGTAACAAATCTGAAGGGAAATCTTAAAGATAATCGTAA 1277
QY 361 GATCACATCGATGGTATCCAAGCCTATCATTGTGATTTGAAACAAATAAAAAATGGTAA 420
D5 1278 GATCACATCGATGGTATCCAAGCCTATCATTGTGATTTGAAACAAATAAAAAATGGTAA 1337
QY 421 ACTGCTTCAAGAATTAGACTATAAGTAGAAATAATTCTACAGATAAGGACTATAT 480
D5 1338 ACTGCTTCAAGAATTAGACTATAAGTAGAAATAATTCTACAGATAAGGACTATAT 1397
QY 481 ACTAATGGACCTCTTAATAATGAAACTGGATAATAAGTCTACCTTAAGATAAGGAA 540
D5 1398 ACTAATGGACCTCTTAATAATGAAACTGGATAATAAGTCTACCTTAAGATAAGGAA 1457
QY 541 AGTTTTTGCTTGTGATTTCCTGAAACCGAATTACTCACTAAATACTTGTGATA 600
D5 1458 AGTTTTTGCTTGTGATTTCCTGAAACGAACTTCACTAAATACTTGTGATA 1517
QY 601 TATAAACATAATGAAACGCTTGTACTCAACACAGCCAAATGCAAGGCTACCTAACACC 660
D5 1518 TATAAACATAATGAAACGCTTGTACTCAACACAGCCAAATGCAAGGCTACCTAACACC 1577
QY 661 AAG 663
D5 1578 AAG 1580

QY ; Sequence 12, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION : MUTANTS OF STREPTOCOCCAL TOXIN A
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308, 830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997

QY ; Application Number: 607038-930
; Filing Date: 06-JBC-1996
; Attorney/Agent Information
; Name: Skoog, Mark T
; Registration Number: 40,178
; Reference/Docket Number: 600.346USW
; Telecommunication Information:
; Telephone: 612-332-5300
; Telex: 612-332-9081
; Information for SEQ ID NO: 12:
; Sequence Characteristics
; Length: 1851 base pairs
; Type: nucleic acid
; Strandness: single
; Topology: linear
; Molecule Type: Genomic DNA
; Feature: Coding Sequence
; Name/Key: Coding Sequence
; Location: 828..1580
; Other Information:
; Sequence Description: SEQ ID NO: 12:
US-09-308-830-12
Query Match Score 100.0%; DB 13; Length 1851;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAACAAGCCCCATCAAGGCCAACCTCACAGCTAGTTAGGTTAAACCTTCATAAAAT 60
Db 918 CAACAAGCCCCATCAAGGCCAACCTCACAGCTAGTTAGGTTAAACCTTCATAAAAT 977
QY 61 ATATATTTCTTATGAGGGTACCCGTACTCAGGAAATGCGAAATCTGTGATCAA 120
Db 978 ATATATTTCTTATGAGGGTACCCGTACTCAGGAAATGCGAAATCTGTGATCAA 1037
QY 121 CTTTATCTCACCTTAATAATGTTGAACTTCACTAAATACTTGTGATA 1457
Db 1038 CTTTATCTCACCTTAATAATGTTGAACTTCACTAAATACTTGTGATA 1097
QY 181 GAACTTAAACAAAGGATGGAACTTTTAACTGATAAACTTGTGAAATGGCAAAATTGGTAA 240
Db 1098 GAACTTAAACAAAGGATGGCAACCTTGTGAAATGGCAAAATTGGTAA 1157
QY 241 GAAAGAATTACCATCTGTATTATGTGAAATGGCAAAATTGGTAA 300
Db 1158 GAAAGAATTACCATCTGTATTATGTGAAATGGCAAAATTGGTAA 1217
QY 301 GGAGGGTAACAAATCTGAAGGGAACTTCAAAAGATACTCGTAA 360
Db 1218 GGAGGGTAACAAATCTGAAGGGAACTTCAAAAGATACTCGTAA 1337
QY 421 ACTAATGGACCTCTTAATAATGAAACTGGATAATAAGTCTACCTAACACC 660
Db 1338 ACTGCTTCAAGAATTAGACTATAAGTAGAAATACTTGTGATA 1577
QY 481 ACTAATGGACCTCTTAATAATGAAACTGGATAATAAGTCTACCTAACACC 540
Db 1398 ACTAATGGACCTCTTAATAATGAAACTGGATAATAAGTCTACCTAACACC 1277
QY 541 AGTTTTTGCTTGTGATTTCCTGAAACCGAATTACTCACTAAATACTTGTGATA 600
Db 1458 AGTTTTTGCTTGTGATTTCCTGAAACGAACTTCACTAAATACTTGTGATA 1517
QY 601 TATAAACATAATGAAACGCTTGTACTCAACACAGCCAAATGCAAGGCTACCTAACACC 660
Db 1518 TATAAACATAATGAAACGCTTGTACTCAACACAGCCAAATGCAAGGCTACCTAACACC 1577
QY 661 AAG 663
Db 1578 AAG 1580

RESULT 3
Sequence 33, Application US/09452599
Patent No. US20020055101A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.
APPLICANT: Ouellette, Marc
APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
Pathogens and Antibiotic Resistance Genes from Clinical
SPECIMENS FOR ROUTINE DIAGNOSIS IN MICRO

CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR FILING DATE: 1995-09-01
PRIOR APPLICATION NUMBER: 08/304,732
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 33
TYPE: DNA
ORGANISM: Streptococcus pyogenes
US-09-452-599-33

Query Match 99.8%; Score 661.4; DB 9; Length 1837;
Best Local Similarity 99.8%; Pred. No. 4.9e-117;
Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGAGCCCCGATCCAAGCCAACTTCAGATCTAGTTAGTAAAACCTTCAAAT 60
904 CAACAGAACCCGATCCAAGCCAACTTCAGATCTAGTTAGTAAAACCTTCAAAT 963

61 ATATATTTCCTTTATAGGGTACCCGTACTCACAGAACTCGTGTGATCAA 120
964 ATATATTTCCTTTATAGGGTACCCGTACTCAAGAGATGTGAATCTGTTGATCAA 1023

121 CTITATCTCACCATTAAATTATAATGTTCAAGGCCAATTATATATAATTAAACT 180
1024 CTTITATCTCAGGATTTAATATAATGTTCAAGGCCAATTATATATAATTAAACT 1083

181 GAACTAAGAACCAAGATGCCAACTTAACTTAAAGATAAAAACCTTGATTTATGGT 240
1084 GAACTAAGAACCAAGATGCCAATTAACTTAAAGATAAAAACCTTGATTTATGGT 1143

241 GTAGAATATTACCATCTCTGTTATTATGCAAATGCAAGGGATGCTGTAACTAC 300
1144 GTAGAATATTACCATCTCTGTTATTATGCAAATGCAAGGGATGCTGTAACTAC 1203

301 GAGGGGTAAACAAATCATGAGGGATCATTTAGAAATTCTAAAGATGTCGTAAA 360
1204 GAGGGGTAAACAAATCATGAGGGATCATTTAGAAATTCTAAAGATGTCGTAAA 1263

361 GTTAACTGATGATGGTATCCAAGCCATCTTGTGATTGAAACAAATGAAATTGGTA 420
1264 GTTAACTGATGATGGTATCCAAGCCATCTTGTGATTGAAACAAATGAAATTGGTA 1323

421 ACTGCTCAAGAATTAGACTAAAGCTTAGAAAAATACCTTACAGATAAAACCTATAT 480
1324 ACTGCTCAAGAATTAGACTAAAGCTTAGAAAAATACCTTACAGATAAAACCTATAT 1383

481 ACTAATGGACCTCTAAATCTGAAACTTAAAGTATAAAGTCATAACCTAAAGATAAGAA 540
1384 ACTAATGGACCTCTAAATCTGAAACTTAAAGTCATAACCTAAAGATAAGAA 1443

541 AGTTTTGGTTGATTCTCCCTGAACTGAGAAATTACTCAATCTATGATA 1503

Db 1578 AAG 1580
QY 661 AAG 663
Db 1564 AAG 1566

RESULT 4
US-10-121-120-33
Sequence 33, Application US/10121120
Publication No. US20030180733A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.
APPLICANT: Ouellette, Marc
APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Specific and Universal Probes and Amplification
Primers
TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
Pathogens and Antibiotic Resistance Genes from Clinical
SPECIMENS FOR ROUTINE DIAGNOSIS IN MICRO

CURRENT APPLICATION NUMBER: US/10/121,120
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 08/452,599
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 1837
TYPE: DNA
ORGANISM: Streptococcus pyogenes
US-10-121-120-33

Query Match 99.8%; Score 661.4; DB 15; Length 1837;
Best Local Similarity 99.8%; Pred. No. 4.9e-117;
Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CACAAAGCCCCATCAAGCCAACTTCAGATCTAGTTAGTAAAACCTTCAAAT 60
904 CACAAAGCCCCATCAAGCCAACTTCAGATCTAGTTAGTAAAACCTTCAAAT 963

61 ATATATTTCCTTTATAGGGTACCCGTACTCACAGAACTCGTGTGATCAA 120
964 ATATATTTCCTTTATAGGGTACCCGTACTCAAGAGATGTGAATCTGTTGATCAA 1023

121 CTITATCTCACCATTAAATTATAATGTTCAAGGCCAATTATATATAATTAAACT 180
1024 CTTITATCTCAGGATTTAATATAATGTTCAAGGCCAATTATATATAATTAAACT 1083

181 GAACTAAGAACCAAGATGCCAACTTAACTTAAAGATAAAAACCTTGATTTATGGT 240
1084 GAACTAAGAACCAAGATGCCAATTAACTTAAAGATAAAAACCTTGATTTATGGT 1143

241 GTAGAATATTACCATCTCTGTTATTATGCAAATGCAAGGGATGCTGTAACTAC 300
1144 GTAGAATATTACCATCTCTGTTATTATGCAAATGCAAGGGATGCTGTAACTAC 1203

301 GAGGGGTAAACAAATCATGAGGGATCATTTAGAAATTCTAAAGATGTCGTAAA 360
1204 GAGGGGTAAACAAATCATGAGGGATCATTTAGAAATTCTAAAGATGTCGTAAA 1263

361 GTTAACTGATGATGGTATCCAAGCCATCTTGTGATTGAAACAAATGAAATTGGTA 420
1264 GTTAACTGATGATGGTATCCAAGCCATCTTGTGATTGAAACAAATGAAATTGGTA 1323

421 ACTGCTCAAGAATTAGACTAAAGCTTAGAAAAATACCTTACAGATAAAACCTATAT 480
1324 ACTGCTCAAGAATTAGACTAAAGCTTAGAAAAATACCTTACAGATAAAACCTATAT 1383

481 ACTAATGGACCTCTAAATCTGAAACTTAAAGTATAAAGTCATAACCTAAAGATAAGAA 540
1384 ACTAATGGACCTCTAAATCTGAAACTTAAAGTCATAACCTAAAGATAAGAA 1443

541 AGTTTTGGTTGATTCTCCCTGAACTGAGAAATTACTCAATCTATGATA 600

Db 1444 AGTTTTGGTTGATTCTCCCTGAACTGAGAAATTACTCAATCTATGATA 1503
QY 601 TATAAGGATATTGAAACGCTTGACTCCTAACAACTGCTACCTAACACC 660
Db 1504 TATAAGGATATTGAAACGCTTGACTCCTAACAACTGCTACCTAACACC 1563

RESULT 5
US-08-882-431-15
; Sequence 15, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRMC -504 Scott Street MCNR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882-431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 2,6,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1837
; TYPE: Nucleic Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: DNA
; US-08-882-431-15

Query Match 99.3%; Score 658.2; DB 8; Length 1837;
Best Local Similarity 99.5%; Pred. No. 2e-116;
Matches 660; Conservate 0; Mismatches 3; Indels 0; Gaps 0;

Query 1 CAAAGAACCCGATCCAGCAACTTCAGATCTAGTTAACCTCAAAAT 60
904 CAACAGAACCCGATCCAGCAACTTCAGATCTAGTTAACCTCAAAAT 963

Qy 61 ATATATTTCCTTGTAGGGTGAACCCCGTTACTCACCGAGAATGTGAATCTGTGATCAA 1.20
Db 964 ATATATTTCCTTGTAGGGTGAACCCCGTTACTCACCGAGAATCTGTGATCAA 1023
Qy 121 CTTTATCCTACCAATTATAATATGTTCAGGCCAAATTATGATAAATTAAACT 180
Db 1024 CTAGATCCTACCAATTATAATGTTCAGGCCAAATTATGATAAATTAAACT 1083
Qy 181 GAATTAAGAACAGAGATGCCAACCTTATAAGGATAAAAAGCTGATATTGTT 240
Db 1084 GAATTAAGAACAGAGATGCCAACCTTATAAGGATAAAAAGCTGATATTGTT 1143
Qy 241 GTGAAATATTACATCTCTGTATTATGTGAATTCAGAAGGAGTCATGTATCTAC 3.0
Db 1144 GTGAAATATTACATCTCTGTATTATGTGAATTCAGAAGGAGTCATGTATCTAC 12.03
Qy 301 GGAGGGTAACAAATCATGAAGGAATATTAGAATTCCAAAAAGATACTCGTAA 3.60
Db 1264 GTATCAATCGATGGTATCCAACCCCTATCAATTGATATTGAAATAATGTTA 13.23
Qy 421 ACTGCTAACAAATTAGACTATAAGTGTAAATTATCTACAGATAATAGCAACTATAT 48.0
Db 1324 ACTGCTAACAAATTAGACTATAAGTGTAAATTATCTACAGATAATAGCAACTATAT 13.83
Qy 481 ACATAATGACCTTAAATATGAACTGGATAACCTTAGATAAGTGTACCTAGATA 54.0
Db 1384 ACTAATGACCTTAAATATGAACTGGATAACCTTAGATAAGTGTAAATGTTA 14.43
Db 541 AGTTTTGGTTGATTTTCCCTGAAACGAGATTACTCAATCTAAATCTATGATA 6.00
Db 1444 AGTTTTGGTTGATTTTCCCTGAAACGAGATTACTCAATCTAAATCTATGATA 15.03
Qy 601 TATAAAGATAAAACGCTTGACTCAAACAGCCAAATGGAAGTCTACCTAACACC 6.60
Db 1504 TATAAAGATAAAACGCTTGACTCAAACAGCCAAATGGAAGTCTACCTAACACC 15.63
Db RESULT 6
US-10-002-784A-15
; Sequence 15, Application US/10002784A
; Publication No. US2003001664A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIORITY APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIORITY FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 15
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-15
Query Match 99.0%; Score 656.6; DB 15; Length 1837;
Best Local Similarity 99.4%; Pred. No. 4.1e-116;
Matches 659; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAAGAACCCGATCCAGCAACTTCAGATCTAGTTAACCTCAAAAT 60
904 CAACAGAACCCGATCCAGCAACTTCAGATCTAGTTAACCTCAAAAT 963

US-09-870-759-19

MS-09-751-708A-19

US-09-870-759-19

Query Match 87.9%; Score 582.6; DB 9; Length 1031;
Best Local Similarity 97.1%; Pred. No. 5e-102;
Matches 636; Conservative 0; Mismatches 14; Indels 5; Gaps 4;

Qy 10 CCCGATCCAGGCAACTTCAGCATCTAGTTAGTAAACCTTCAAATATAATT 69
Db 178 CCCAGGCCAGCAATTACAAGATCTAATTAGTT AAAACCTTCAAATATAATT 236

Qy 70 CTTATGAGGTGACCT - GTTACTCTACGGAACTTGATCAACTTTATC 128
Db 237 CTTATGAGGTGACCCGTGACTACGAGATGTAACTTGTAACTTTATC 296

Qy 129 TCACTTAAATATAATGTTCAGGGCCAATTATGATAAACTGAACTAA 188
Db 297 ACACGTTAAATATAATGTTCAGGGCCAATTATGATAAACTGAACTAA 356

Qy 189 GAACCAAGAGATGGCAACTTATTAGTAAACCTGGATATGGTTAGATA 248
Db 357 GAACCAAGAGATGGCAACTTATTAGTAAACCTGGATATGGTTAGATA 416

Qy 249 TTACCATCTCGTTAATTATGTGAAAATGGCAACTTACCGGGGT 308
Db 417 TTACCATCTCGTTAATTATGTGAAAATGGCAACTTACCGGGGT 476

Qy 309 AACAAATCATGAAGGGATCATTGAAATCTCAAGCTTAAGTCAAT 368
Db 477 AACAAATCATGAAGGGATCATTGAAATCTCAAGCTTAAGTCAAT 536

Qy 369 CGATGGTATCCAAGCCTATATTGAAATAAAAGTAGTCGTCA 428
Db 537 CGATGGTATCCAAGCCTATATTGAAATAAAAGTAGTCGTCA 594

Qy 429 AGAATTAGACTATAAGTAAAGTAACTTACGATAATAAGCRACTATACTATGG 488
Db 595 AGAATTAG - CATACTAGTTGAAATACTCTACGATAATAAGCRACTATACTATGG 653

Qy 489 ACCCTCTAAATATGAACTGATATAAGTCTACCTAAGATAAAAGAGTTTG 548
Db 654 ACCCTCTAAATATGAACTGATATAAGTCTACCTAAGATAAAAGAGTTTG 713

Qy 549 GTTGTGTTTCCCTGAAACCGAGATTACTCACTAAATCTATGATAATAAGA 608
Db 714 GTTGTGTTTCCCTGAAACCGAGATTACTCACTAAATCTATGATAATAAGA 773

Qy 609 TAATGAAACGGCTGACTCTAACACAGCCAAATTGAAAGTCTACCTAACACCAAG 663
Db 774 TAATGAAACGGCTGACTCTAACACAGCCAAATTGAAAGTCTACCTAACACCAAG 828

RESULT 9
US-09-751-708A-19
Sequence 19, Application US/09/751-708A
Publication No. US2003157113A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751-708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 19
LENGTH: 1031
FEATURE: DNA
NAME/KEY: CDS
ORGANISM: Streptococcus pyogenes
OTHER INFORMATION:

RESULT 10
US-09-870-759-11
Sequence 11, Application US/09/870-759
Patent No. US2002177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 70759
CURRENT APPLICATION NUMBER: US/09/870-759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 11
LENGTH: 1095
TYPE: DNA
ORGANISM: staphylococcus aureus
FEATURE:
NAME/KEY: CDS
LOCATION: (118)..(918)
OTHER INFORMATION:

US-09-870-759-11

US-09-751-708A-11

Query Match 25.2%; Score 167.4; DB 10; Length 1095;
 Best Local Similarity 59.0%; Pred. No. 1.7e-22;
 Matches 382; Conservative 0; Mismatches 226; Indels 39; Gaps 4;

QY 56 AAAATATAATTCTCTTATGAGGGTGAACCTGTACTCACGAGATGTAAATCTGTTG 115
 Db 263 AAAATGAAAGTTTATATGATCATATGATCAACTARAGTAAAGTCGTG 322

QY 116 ATCAACTTTCATCTCACCCTTAATATATAATGTTCAGG-----GCCAAATTATG 166
 Db 323 ATAATTTTGCCATGATTTAATTAACATAGTATRAAAACGAAATTATG 382

QY 167 ATAAATTAAAACCTGAACTTAGACCAAGAAAGTGGCACTTATTAAGGATAAAGC 226
 Db 383 ACAAAAGTGGAAAACAGAGTTAAATGAGGTAAAGAAGTAAAGATGAACTAG 442

QY 227 TTGATATTATGGTGTAGAAATTACATCTCGTTATTAT-----268
 QY 443 TTGATGTGTGTGATCAGAACATTACTATGAAACCTTTCATCCAAAGATTAATG 502
 Db 503 GTGAAAATGCGAAAGGGTGCATGTATCTACGGAGGGTAACAATCTGAACGGAAATC 328
 QY 329 ATTAGAATTCCTA----AMAGTAACTCGTTAAAGTATCATCGTGTATCCAA 382
 Db 563 ACTTGATATGGGAACCTACAATGGTTATCAAATAAAGAAACA 622

QY 383 GCCTATCATTTGATATGGAAACAAATAAAAATGTAAGGTTAACGTTAACATTA 442
 Db 623 CAATTCCTTGTGATGCGAACCTATRABAAAAGTCAAGCTAACGACTAACATA 682

QY 443 AAGTTGAAATAATCTTACGATAAACTGAAACTATACATGTTAACGTTAACATTA 502
 Db 683 AAAGCTGGATTTTAAATTAATAAAAATTTGATGTTAACGTTAACGTTAACATATG 742

QY 503 AAACCTGGATATAAAGTCTACCTAACGATAAGGAAATGGTAAAGTGTAAAGCTAACATA 562
 Db 743 AAACAGGATATAAAATTATTTGAAATAACGGAAATTTGGTTGATGATGTC 802

QY 563 CTGAAACCG-----AATTTACTCATCTAAATCTTATGATAATAAGATATGAA 616
 Db 803 CTGCACCGGGATAGTTGACCAATTTGACGATCAAGACATAAA 862

QY 617 CGCTTGACTCAACACAGCCAAATTGAAAGTCTACCTAACACCCAG 663
 Db 863 CGGTGATCTTAAAGTGTGAGATAGAAGTCCACCTAACACAG 909

RESULT 11

US-09-751-708A-11
 Sequence 11, Application US/09751-708A
 Publication No. US2003015713A1
 GENERAL INFORMATION:
 APPLICANT: TERMAN, David S.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 CURRENT APPLICATION NUMBER: US/09/751,708A
 PRIORITY FILING DATE: 2002-10-15
 NUMBER OF SEQ ID NOS: 166
 SEQ ID NO 11
 LENGTH: 1095
 TYPE: DNA
 ORGANISM: *Staphylococcus aureus*
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: (118) .. (918)
 OTHER INFORMATION:

RESULT 12

US-10-354-948-1
 Sequence 1, Application US/10354948
 Publication No. US2003020262A1
 GENERAL INFORMATION:
 APPLICANT: Elmslie, Robyn E.
 TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sheridan Ross & McIntosh
 STREET: 1700 Lincoln Street, Suite 3500
 CITY: Denver
 STATE: Colorado
 COUNTRY: U.S.A.
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.2.5

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/354, 948
 FILING DATE: 29-Jan-2003
 CLASSIFICATION: 4,24
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32,020
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELEX/FAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 773 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..768
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-354-948-1.

Query Match 25.2%; Score 166.8; DB 13; Length 773;
 Best Local Similarity 59.1%; Pred. No. 1..9e-22;
 Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;

Qy 56 AAAATAATATTTCTTTATGAGGTGACCCCTGTACTCAGAAGTGTGAATCTGTG 115
 Db 113 AAAATATGAAGTTCTATGATGAAATCATGTATCAGCAATAACGTTAACATAG 172
 Qy 116 ATCAAATTTCATCTCACATTAAATATAATGGTCAAGGCACCA-----AAATTAG 166
 Db 173 ATCAATTTCATACTTGACTTAATATCTTAAATATATGTTAACGGCAATTATG 232
 Qy 167 ATAAATTTAAACTGAACTTAAAGGACACTAACTAAGGTTAACGGAAATTATG 226
 Db 174 ATCAATTTCATACTTGACTTAATATCTTAAATATATGTTAACGGCAATTATG 232
 Qy 227 TTGATATTATGGTGTAGAATAATCCATCTCGTTAAATTAGTGAATA----- 275
 Db 266 ATAATGTCGAGTCGAAATTAAAACAGATTAGGTGATAATAAAAGATAACAG 325
 Qy 228 TTGATATTATGGTGTAGAATAATCCATCTCGTTAAATTAGTGAATA----- 275
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 Qy 614 AACGCTGTAACCTCAAAACAGCAAAATGGAAAGTCACTAACACCAAG 663
 Db 743 AAATGGTTGATCTAAAGTAAATCTGAAATGTTAACGGAAATGTTAACGGAAAG 792

RESULT 13
 US-09-870-759-1
 Sequence 1, Application US/09870759
 Patent No. US20020177551A1
 GENERAL INFORMATION:
 APPLICANT: TERMIN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870-759
 CURRENT FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 1
 LENGTH: 801
 TYPE: DNA
 ORGANISM: *Staphylococcus sp.*
 US-09-870-759-1

Query Match 25.2%; Score 166.8; DB 9; Length 801;
 Best Local Similarity 59.1%; Pred. No. 2e-22;
 Matches 384; Conservative 0; Mismatches 221; Indels 45; Gaps 4;

Qy 56 AAAATAATATTTCTTTATGAGGTGACCCCTGTACTCAGAAGTGTGAATCTGTG 115
 Db 146 AAAATAGAAACGTTCTATGATGATAATGAACTTAAATCTAATGATA 205
 Qy 116 ATCAAACPTTAAATCTCACATTAAATATAATGTTAGGGCA-----AAATTAG 166
 Db 206 ATCAAATTCATACTTGACTTAATATTCTTAAAGGACACTAAAGTGGAAATTAG 265
 Qy 167 ATAAATTTAAACTGAACTTAAAGAAGATGGCACTTAAATAGGATAAAACAG 226
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 Qy 276 -----TGCAGAAAGGAGTGGCTGAAATGAACTTAAAGGTTAACCAATCATG 319
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 Db 446 ATGGAAACCAATTAGATAATATAGAGTATCTGTTGCAAGTGGTATCTGTTAACGGAAATGATA 505
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 Db 506 ATTATATCCTTGGACTTAATATGAAATGTTAACGGAAATGTTAACGGAAATGATA 565
 Qy 440 ATAAAGTTGAAATAATCTTCAGATAATAGCAACTATATACATAATGGCACTCTAAAT 499
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 Qy 560 TCCCTGAACTGACTTAAATCTGAAATGTTAACGGAAATGTTAACGGAAATGATA 559
 Db 683 TCCCTGAACTGACTTAAATCTGAAATGTTAACGGAAATGTTAACGGAAATGATA 742
 Qy 614 AACGCTGTAACCTCAAAACAGCAAAATGGAAAGTCACTAACACCAAG 663
 Db 743 AAATGGTTGATCTAAAGTAAATCTGAAATGTTAACGGAAATGTTAACGGAAAG 792

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RESULT 15
US-09-870-759-2
; Sequence 2, Application US/09870759
; Patent No. US2002017751A1
; GENPAT INFORMATION.

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